

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:35:27 ; Search time 170 Seconds
(without alignments)
1114.525 Million cell updates/sec

Title: US-10-606-055-2
Perfect score: 370
Sequence: 1 MRLIFVYTLICANFCSCRD.....DIQLDHERCDCICSSRPPR 370

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 5

Total number of hits satisfying chosen parameters: 93916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	370	2 Q9GZP0	Q9GZP0 homo sapien
2	323	87.3	364	2 Q9BMV5	Q9BMV5 homo sapien
3	35	9.5	300	2 Q6V9H4	Q6V9H4 oryctolagus
4	32	8.6	370	2 Q9EQT1	Q9EQT1 rattus norv
5	27	7.3	261	2 Q8K2L3	Q8K2L3 mus musculus
6	27	7.3	370	2 Q925I7	Q925I7 mus musculus
7	9	2.4	77	2 Q93X22	Q93X22 quercus sub
8	9	2.4	77	2 Q75NH6	Q75NH6 pisum sativ
9	9	2.4	79	2 Q9ZRV0	Q9ZRV0 fagus sylv
10	8	2.2	76	2 Q22492	Q22492 oenanthel
11	8	2.2	76	2 Q22581	Q22581 pimpinella
12	8	2.2	76	2 Q9M4N0	Q9M4N0 persea amer
13	8	2.2	77	1 MT2_VICFA	Q41657 vicia faba
14	8	2.2	77	1 MTA_TRIRP	P43398 trifolium r
15	8	2.2	77	2 Q8S3M2	Q8S3M2 azolla fili
16	8	2.2	77	2 Q6I674	Q6I674 citrullus l
17	8	2.2	77	2 Q9AR26	Q9AR26 avicennia m
18	8	2.2	77	2 Q9SNGT3	Q9SNGT3 eichornia
19	8	2.2	77	2 Q9ZNTG5	Q9ZNTG5 eichornia
20	8	2.2	78	1 MT2_NICGU	Q40396 nicotiana g
21	8	2.2	78	2 Q93WV3	Q93WV3 narcissus p
22	8	2.2	78	2 Q94G67	Q94G67 amarantus
23	8	2.2	78	2 Q6L8H8	Q6L8H8 codonopsis
24	8	2.2	78	2 Q6PML3	Q6PML3 populus bal
25	8	2.2	78	2 Q8GTD0	Q8GTD0 hordeum vul
26	8	2.2	79	1 MT2_CICAR	Q39459 cicer ariet
27	8	2.2	79	2 Q80335	Q80335 citrullus unsh
28	8	2.2	79	2 Q944W1	Q944W1 typha latif
29	8	2.2	79	2 Q6PML4	Q6PML4 populus bal
30	8	2.2	79	2 Q75NH4	Q75NH4 dolichos la
31	8	2.2	79	2 Q75NH9	Q75NH9 phaseolus a

Q75NI1	glycine max	79	2	Q75NI1
Q75NI3	phaseolus a	79	2	Q75NI3
Q7M213	glycine max	79	2	Q7M213
Q9AUL6	typha latif	79	2	Q9AUL6
Q9AXE5	avicennia m	79	2	Q9AXE5
Q9FQ79	musa acumin	79	2	Q9FQ79
P43396	coffee arab	80	1	MT1_COPAR
P56168	brassica ju	80	1	MT21_BRAJU
P56170	brassica ju	80	1	MT23_BRAJU
P56172	brassica ju	80	1	MT25_BRAJU
Q42494	brassica ra	80	1	MT2_BRARA
Q39269	brassica ra	80	1	MT2_BRARP
P30564	ricinus com	80	1	MT2_RICCO
O04107	oryza sativ	80	2	O04107
O04688	mesembryant	80	2	O04688
O22488	oryza sativ	80	2	O22488
Q7XAF3	pringlea an	80	2	Q7XAF3
Q8GTC9	hordeum vul	80	2	Q8GTC9
Q9FR40	petunia hyb	80	2	Q9FR40
Q9M697	brassica ol	80	2	Q9M697
P25860	arabidopsis	81	1	MT2A_ARATH
Q6J9F8	xerophyta h	81	2	Q6J9F8
O6P24	cynodon dac	81	2	O6P24
P94029	oryza sativ	82	1	MT21_ORYSA
Q40158	lycopersico	82	1	MT2B_LYCES
Q7F7X9	oryza sativ	82	2	Q7F7X9
Q9SPE7	ipomoea bat	82	2	Q9SPE7
P93433	oryza sativ	84	1	MT22_ORYSA
O65XV5	oryza sativ	84	2	O65XV5
Q7X9M0	triticum ae	84	2	Q7X9M0
Q8XIQ7	clostridium	114	2	Q8XIQ7
Q94CT9	oryza sativ	124	2	Q94CT9
Q9F8C4	streptococc	136	2	Q9F8C4
Q8ELC6	streptococc	174	2	Q8ELC6
Q8S6U3	streptococc	174	2	Q8S6U3
Q84684	peanut chlo	174	2	Q84684
Q9NRA1	homo sapien	220	2	Q9NRA1
Q9UI22	homo sapien	345	2	Q9UI22
Q9EQX6	rattus norv	345	2	Q9EQX6
Q9JHV8	mus musculu	345	2	Q9JHV8
Q9QV71	m fallotein	345	2	Q9QV71
Q8C119	mus musculu	345	2	Q8C119
Q9I946	gallus gall	345	2	Q9I946
Q8Y7C9	listeria mo	353	2	Q8Y7C9
Q92C00	listeria in	353	2	Q92C00
Q71ZM8	listeria mo	353	2	Q71ZM8
P21307	zymomonas m	485	1	G6PD_ZYMMO
Q49067	zea mays (m	531	2	Q49067
Q76267	bacterioph	772	2	Q76267
Q8I734	trypanosoma	850	2	Q8I734
P91638	drosophila	935	2	P91638
Q9VS62	drosophila	944	2	Q9VS62
Q8Y469	listeria mo	995	2	Q8Y469
Q927Q7	listeria in	995	2	Q927Q7
Q71WJ3	listeria mo	995	2	Q71WJ3
Q7Q5U3	anopheles g	1072	2	Q7Q5U3
TIE1_HUMAN	homo sapien	1138	2	TIE1_HUMAN
O86AS3	dicystosteli	1318	2	O86AS3
Q8GSP2	streptomyce	1318	2	Q8GSP2
Q65VA7	mannheimia	35	2	Q65VA7
Q9US55	schizosacch	66	2	Q9US55
O22319	musa acumin	78	1	MT2_MUSAC
Q94198	atropha bell	96	2	Q94198
Q95R16	caenorhabdi	96	2	Q95R16
Q8H9H2	lactococcus	98	2	Q8H9H2
Q7XHJ3	quercus rob	98	2	Q7XHJ3
Q7PE07	anopheles g	99	2	Q7PE07
Q94M87	lactococcus	99	2	Q94M87

ALIGNMENTS

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RESULT 1
Q9GZP0
ID Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (NSTP036) (Platelet-derived growth
factor D) (Iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
OC Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11125282; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
EX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA Laroche W.J., Jeffers M., McDonald W.F., Challakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881; DOI=10.1038/35074588;
RA Bergstein E., Uetela M., Li X., Pietras K., Ostman A., Heidin C.H.,
RA Allitalo K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
DR EMBL; AB033832; BAB18903.1; -
DR EMBL; AF113216; AAG39287.1; -
DR EMBL; AF335584; AAK38840.1; -
DR EMBL; AF336376; AAK56136.1; -
DR EMBL; AY027517; AAK20081.1; -
DR PIR; JC7591; JC7591.
DR HSSP; Q9JUS8; 1N70.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD growth factor.
DR Efam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF 2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 370 AA; 42948 MW; D387F485E7BB7674_CRC64;
Query Match 100.0%; Score 370; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLYRDETIOVKG 60
DB 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLYRDETIOVKG 60
QY 61 NGYVQSPFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLSEANDICRYDFVEVEDIS 120
DB 61 NGYVQSPFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLSEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCGHKHEVPPRIKSRNTQIKITFKSDDYFVAKFGFKIYYSLLEDQFQAAASE 180
DB 121 ETSTIIRGRWCGHKHEVPPRIKSRNTQIKITFKSDDYFVAKFGFKIYYSLLEDQFQAAASE 180
QY 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWQEDLENNY 240
DB 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCYTPRNYSVNIREELKLANVVFFPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCYTPRNYSVNIREELKLANVVFFPRCLLVQ 300
QY 301 RCGNGCGGTVNRWRSCTNSGKTVKKYHEVLFQFPGHKKRGRKTMALVDIQLDHHERC 360
DB 301 RCGNGCGGTVNRWRSCTNSGKTVKKYHEVLFQFPGHKKRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPPR 370
DB 361 DCICSSRRPPR 370
RESULT 2
Q9BWV5
ID Q9BWV5 PRELIMINARY; PRT; 364 AA.
AC Q9BWV5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Iris-expressed growth factor short form (Platelet derived growth
factor D, isoform 2) (SCDGF-B).
GN Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grichwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maria M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Testis;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY027518; AAK20082.1; -;
DR EMBL; BC030645; AAH30645.1; -;
DR EMBL; AY359116; AAQ89474.1; -;
DR PIR; JC7591; JC7591.
DR HSSP; Q9JJS8; 1NTO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;
DR HSSP; Q9JJS8; 1NTO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
Query Match 87.3%; Score 323; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 DLYRRDETQVKGNGVQSPFPNSYPRNLLTTLRLHSGENTRIQLVFNQFGLAEAND 107
DB 42 DLYRRDETQVKGNGVQSPFPNSYPRNLLTTLRLHSGENTRIQLVFNQFGLAEAND 101
QY 108 ICRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYY 167
DB 102 ICRYDFVEVEDISETSTIIRGRWCGHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYY 161
QY 168 SLEDFQPAASSETNWESVTSSISGVSYNSPSTVDPTLLADALDKIAEFDVTELLKYF 227
DB 162 SLEDFQPAASSETNWESVTSSISGVSYNSPSTVDPTLLADALDKIAEFDVTELLKYF 221
QY 228 NPESMQEDLENMYLDTPRYGRGRSYHDKSKVDLDRNLDDAKRYSCPTPRNYSNIREELKL 287
DB 222 NPESMQEDLENMYLDTPRYGRGRSYHDKSKVDLDRNLDDAKRYSCPTPRNYSNIREELKL 281
QY 288 ANWFFPRCLLVQRCGCGCGCTVNRSCITSCNGKTVKKYHEVLOFEPGHIKRRGRAKTM 347
DB 282 ANWFFPRCLLVQRCGCGCGCTVNRSCITSCNGKTVKKYHEVLOFEPGHIKRRGRAKTM 341
QY 348 ALVDIQLDHHERCDCICSRPPR 370
DB 342 ALVDIQLDHHERCDCICSRPPR 364
ID Q6V9H4 PRELIMINARY; PRT; 300 AA.
AC Q6V9H4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Iris-expressed growth factor (Fragment).
GN Name=PDGFD;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Ray S., Wistow G.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;
Query Match 9.5%; Score 35; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 YRGRSYHDKSKVDLDRNLDDAKRYSCPTPRNYSVN 280
DB 190 YRGRSYHDKSKVDLDRNLDDAKRYSCPTPRNYSVN 224
ID Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=rSCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RL SCDGF/PDGF-C/fallicotin";
DR EMBL; AB052170; BAB18920.1; -;
DR PIR; JC7592; JC7592.
DR HSSP; Q9UCV4; 1NZI.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.

DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS0278; PDGF; 2; 1.
 SQ SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73 CRC64;

Query Match 8.6%; Score 32; DB 2; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4.4e-24;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ATPQASIKALRNANLRDESNHLDLYRRDE 54
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 DB 23 ATPQASIKALRNANLRDESNHLDLYRRDE 54

RESULT 5

ID Q8K2L3 PRELIMINARY; PRT; 261 AA.
 AC Q8K2L3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pdgd protein.
 GN Name=Pdgd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030896; AAH30896.1; -.
 DR HSSP; Q9JUS8; INT0.
 DR MGD; MG1:1919035; Pdgd.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IDA.
 DR InterPro; IPR000859; CUB.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR PROSITE; PS01180; CUB; 1.
 SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F6373A52D09 CRC64;

Query Match 7.3%; Score 27; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 5.1e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 142 SRTNQIKITKSDDDYFVAKGCFKIYYS 168
 |||||
 DB 142 SRTNQIKITKSDDDYFVAKGCFKIYYS 168
 |||||
 RESULT 6
 Q92517 PRELIMINARY; PRT; 370 AA.
 ID Q92517; Q9DIL8;
 AC Q92517; Q9DIL8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Platelet-derived growth factor D (Mus musculus 18-day embryo whole
 body cDNA, RIKEN full-length enriched library, clone:1110003I09
 product:platelet-derived growth factor D).
 DE Name=Pdgd;
 GN Name=Pdgd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
 RA LaChelle W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
 RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
 RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
 RA Shimkets R.A., Rothberg J.M., Lichtenstein H.S.;
 RT "PDGF D, A Novel Protease-Activated Growth Factor.";
 RL Nat. Cell Biol. 3:517-521 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcription Research Group Phase I & II Team;
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RESULT 8	Q75NH6	PRELIMINARY;	PRT;	77 AA.
ID	Q75NH6			
AC	Q75NH6;			
DT	05-JUL-2004 (TReMBLrel. 27, Created)			
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DE	Type 2 metallothionein.			
DE	GN	Name=MET;		
OS	Pisum sativum (Garden pea).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosoids			
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.			
OX	NCBI_TaxID=3888;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sun X., Xian X., Hong K., Kajuchi T.;			
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB176565; BAD18383.1; -			
DR	GO; GO:0046872; F:metal ion binding; IEA.			
DR	InterPro; IPR000347; Metallothion_15p.			
DR	Pfam; PF01439; Metallothio_2; 1.			
DR	ProDom; PD001611; Metallothion_15p; 1.			
SQ	SEQUENCE 77 AA; 7728 MW; 7D7911A020BD903C CRC64;			
Query Match	2.4%;	Score 9;	DB 2;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 0.88;		
Matches	9;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	302 CGGCGCGGT 310			
DB				
	4 CGGCGCGGT 12			
RESULT 9	Q9ZRV0	PRELIMINARY;	PRT;	79 AA.
ID	Q9ZRV0			
AC	Q9ZRV0;			
DT	01-MAY-1999 (TReMBLrel. 10, Created)			
DT	01-MAY-1999 (TReMBLrel. 10, Last sequence update)			
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)			
DE	Metallothionein-like protein class II.			
DE	Fagus sylvatica (Beechnut).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosoids			
OC	eurosid1; Fagales; Fagaceae; Fagus.			
OX	NCBI_TaxID=28930;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Seeds;			
RX	MEDLINE=99372458; PubMed=1047467;			
RX	Calvo A.P., Lorenzo O., Nicolas C., Nicolas G., Rodriguez D.;			
RT	"Characterization of a Metallothionein-coding cDNA (Accession No.			
RT	RT AJ130886) from Fagus sylvatica L. seeds. (FGR99-073).";			
RL	Plant Physiol. 120:633-633(1999).			
DR	EMBL; AJ130886; CAA10232.1; -			
DR	GO; GO:0046872; F:metal ion binding; IEA.			
DR	InterPro; IPR000347; Metallothion_15p.			
DR	Pfam; PF01439; Metallothio_2; 1.			
DR	ProDom; PD001611; Metallothion_15p; 1.			
SQ	SEQUENCE 79 AA; 7773 MW; 6936D779AF6D6C4A CRC64;			
Query Match	2.4%;	Score 9;	DB 2;	Length 79;
Best Local Similarity	100.0%;	Pred. No. 0.9;		
Matches	9;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	302 CGGCGCGGT 310			
DB				
	4 CGGCGCGGT 12			

```
RESULT 10
O22492 PRELIMINARY; PRT; 76 AA.
AC O22492;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-1 like protein.
OS Oenanthae javanica (water celery) (Water dropwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Apiales; Apiaceae; Apioidae; Oenantheae; Oenanthe.
OX NCBI_TaxID=49556;
RN [1]
RP SEQUENCE FROM N.A.
RA Min B., Lee S.Y.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017787; AAB70560.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
SQ SEQUENCE 76 AA; 7319 MW; DDF0A352D9448404 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 11
O82581 PRELIMINARY; PRT; 76 AA.
AC O82581;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-1-like protein.
OS Pimpinella brachycarpa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Apiales; Apiaceae; Apioidae; apioid superclade;
OC Pimpinella clade; Pimpinella.
OX NCBI_TaxID=45043;
RN [1]
RP SEQUENCE FROM N.A.
RA Cho J.-I., Lee K.-W.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF093585; AAC62510.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
SQ SEQUENCE 76 AA; 7419 MW; B80BFD32D95892D8 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 12
Q9M4N0 PRELIMINARY; PRT; 76 AA.
AC Q9M4N0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
SQ SEQUENCE 76 AA; 7730 MW; 7D7BAD8D0223BF3C CRC64;

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-like protein type 2 (Fragment).
GN Name=mt2;
OS Persea americana (Avocado).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Persea.
OX NCBI_TaxID=3435;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissot=fruit mesocarp;
RA Zamorano J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D.,
RA Merodio C., Grieron D.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133145; CAB77242.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
FT NON TER 1
SQ SEQUENCE 76 AA; 7568 MW; A6433B2965E1566D CRC64;

Query Match 2.2%; Score 8; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 1 CGGNCGCG 8

RESULT 13
MT2_VICFA STANDARD; PRT; 77 AA.
AC Q41657;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Metallothionein-like protein type 2.
GN Name=MTI;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95036014; PubMed=7948889;
RA Foley R.C., Singh K.B.;
RT "Isolation of a Vicia faba metallothionein-like gene: expression in
RT foliar trichomes."
RT Plant Mol. Biol. 26:435-444(1994).
CC -!- FUNCTION: Metallothioneins have a high content of cysteine
CC residues that bind various heavy metals.
CC -!- TISSUE SPECIFICITY: Expressed in the left, stem and flower, at
CC very low levels in roots and is not detectable in mesophyll
CC protoplasts.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 15.
CC
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CC
CC EMBL; X77254; CAA54471.1; -.
DR PIR; S52636; S52636.
DR InterPro; IPR000347; Metalthion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metalthion_15p; 1.
DR Metal-binding; Metal-thiolate cluster; Multigene family.
SQ SEQUENCE 77 AA; 7730 MW; 7D7BAD8D0223BF3C CRC64;
```

```
Query Match          2.2%; Score 8; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 14
MTA_TRIP
ID MTA_TRIP STANDARD; PRT; 77 AA.
AC P43398;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metallothionein-like protein A (MT-A).
GN Name=MTA;
OS Trifolium repens (Creeping white clover).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trifolium.
OX NCBI_TaxID=3899;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Huia; TISSUE=stolon node;
RA Ellison N.W.; White D.W.R.;
RT "Isolation of two cDNA clones encoding metallothionein-like proteins
from Trifolium repens L.";
RT (er) Plant Gene Register PGR96-068.
CC -!- FUNCTION: Metallothioneins have a high content of cysteine
residues that bind various heavy metals.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 15.
CC -----
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CC -----
DR EMBL; Z26492; CAA81264.1; -
DR PIR; S37239; S37239.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
KW Metal-binding; Metal-thiolate cluster; Multigene family.
SQ SEQUENCE 77 AA; 7503 MW; 5F4C163BA644B8D1 CRC64;

Query Match          2.2%; Score 8; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 15
Q8S3M2
ID Q8S3M2 PRELIMINARY; PRT; 77 AA.
AC Q8S3M2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-like protein 2.
GN Name=A2MT2;
OS Azolla filiculoides (Water fern).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Monilliformopses; Filicophyta; Filicopsida; Hydropteridales;
OC Azollaceae; Azolla.
```

```
OX NCBI_TaxID=84609;
RN [1]
RP SEQUENCE FROM N.A.
RA Schor T.; Goldsbrough P.B.; Adam Z.; Tel-Or E.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF482470; AAL85416.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
SQ SEQUENCE 77 AA; 7839 MW; 54DDF0CC032F50D5 CRC64;

Query Match          2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 16
Q6I674
ID Q6I674 PRELIMINARY; PRT; 77 AA.
AC Q6I674;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type-2 metallothionein.
GN Name=CLMT2;
OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
OX NCBI_TaxID=3654;
RN [1]
RP SEQUENCE FROM N.A.
RA Akashi K.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB182918; BAD26571.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 77 AA; 7805 MW; 6E75AB740535B64 CRC64;

Query Match          2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGCG 309
   |||||
Db 4 CGGNCGCG 11

RESULT 17
Q9AR26
ID Q9AR26 PRELIMINARY; PRT; 77 AA.
AC Q9AR26;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Class I type 2 metallothionein.
OS Avicennia marina (Grey mangrove).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Acanthaceae; Acanthaceae; Acanthaceae; Acanthaceae; Acanthaceae;
OX NCBI_TaxID=82927;
RN [1]
RP SEQUENCE FROM N.A.
RA Parani M.; Parida A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
```

Query Match 2.2%; Score 8; DB 1; Length 78;

```
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 21
Q93W33 PRELIMINARY; PRT; 78 AA.
AC Q93W33;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein-like protein type 2.
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Narcissus.
OC NCBI_TaxID=39639;
RN [1]
RC TISSUE=Senescing tepals of 4-day old flowers;
RC SEQUENCE FROM N.A.
RA Hunter D.A., Steele B.C., Reid M.S.;
RT Identification of genes associated with perianth senescence in
RL Plant Sci. 163:13-21(2002).
DR EMBL; AF420017; AAL16908.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7708 MW; 149B73425AEDB321 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 22
Q94G67 PRELIMINARY; PRT; 78 AA.
AC Q94G67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Metallothionein.
OS Amaranthus cruentus (Purple amaranth).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Amaranthus.
OC NCBI_TaxID=117272;
RN [1]
RC SEQUENCE FROM N.A.
RA Xu F.-X., Sun M.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF268027; AAK57884.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7772 MW; 9CA27DBA2B2992C CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 23
Q6L8H8 PRELIMINARY; PRT; 78 AA.
AC Q6L8H8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Metallothionein 2.
OS Codonopsis lanceolata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Campanulaceae; Codonopsis.
OC NCBI_TaxID=103999;
RN [1]
RC TISSUE=Branch;
RC SEQUENCE FROM N.A.
RA In J.G., Yang D.C., Lee B.S.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB126057; BAD18924.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7826 MW; F8F087DC825F39B6 CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 24
Q6PML3 PRELIMINARY; PRT; 78 AA.
AC Q6PML3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Metallothionein 2b.
GN Name=Mt2b;
OS Populus balsamifera subsp. trichocarpa x Populus deltoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids I; Malpighiales; Salicaceae; Saliceae; Populus.
OC NCBI_TaxID=3695;
RN [1]
RC SEQUENCE FROM N.A.
RA Kohler A., Blande D., Chalot M., Martin F.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY594298; AAT02525.1;
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR ProDom; PD001611; Metallothion_15p; 1.
SQ SEQUENCE 78 AA; 7901 MW; B43DECB278B82ADD CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 CGGNCGCG 309
Db 4 CGGNCGCG 11

RESULT 25
```

Q8GTD0
ID Q8GTD0 PRELIMINARY; PRT; 78 AA.
AC Q8GTD0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Metallothioneine type2.
GN Name=mt2a;
OS Hordeum vulgare var. distichum (Two-rowed barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=112509;
RN [1]_TaxID=112509;
RP SEQUENCE FROM N.A.
RC TISSUE=Primary leaf;
RA Heise J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511345; CAD54079.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000347; Metallothion_15p.
DR Pfam; PF01439; Metallothio_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
SQ SEQUENCE 78 AA; 7312 MW; 47498C0125352A3B CRC64;

Query Match 2.2%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred.No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGG 309
Db 4 CGGNCGG 11
|||||||
|||||||

Search completed: November 10, 2005, 09:46:49
Job time : 174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:20:26 ; Search time 54.2774 Seconds
(without alignments)
805.195 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370

Perfect score: 631

Sequence: 1 VDLDRNLNDKRYSCPRNY.....DIQLDHERCDCICSSRPPR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	123	7	Adk68116 Novel NOV
2	631	100.0	123	8	Adr49105 Human NOV
3	631	100.0	132	4	Aau00699 Human FCT
4	631	100.0	132	5	Abb79644 Human FCT
5	631	100.0	132	5	Abg78503 Human FCT
6	631	100.0	132	7	Adk68112 Novel NOV
7	631	100.0	132	8	Adm57645 Human FCT
8	631	100.0	132	8	Adr49101 Human NOV
9	631	100.0	152	4	Abb11697 Human FCT
10	631	100.0	154	4	Aau00702 Human FCT
11	631	100.0	154	5	Abb79647 Human FCT
12	631	100.0	154	8	Adm57651 Human FCT
13	631	100.0	302	6	Abu72441 ZVEGF4-re
14	631	100.0	302	8	Adj32807 Fusion pr
15	631	100.0	316	6	Abu72442 ZVEGF4-re
16	631	100.0	316	8	Adj32808 Fusion pr
17	631	100.0	317	6	Abg75790 Human gro
18	631	100.0	322	3	Aay71129 Human pla
19	631	100.0	347	7	Adk68120 Novel NOV
20	631	100.0	347	8	Adr49109 Human NOV
21	631	100.0	358	5	Aae15852 Human mat
22	631	100.0	364	4	Aau12264 Human PRO
23	631	100.0	364	5	Aae15820 Human LP8
24	631	100.0	364	5	Abb84973 Human PRO
25	631	100.0	364	5	Abb95579 Human ang

26	631	100.0	364	6	ABO17708	Abol17708	Novel	hum
27	631	100.0	364	6	ABU60962	Abu60962	Human	PRO
28	631	100.0	364	6	ABU66662	Abu66662	Human	PRO
29	631	100.0	364	6	ABU59743	Abu59743	Novel	sec
30	631	100.0	364	6	ABO24933	Abu24933	Human	sec
31	631	100.0	364	6	ABU66938	Abu66938	Human	sec
32	631	100.0	364	6	ADA5705	Ada5705	Novel	hum
33	631	100.0	364	6	ADA76136	Ada76136	Human	PRO
34	631	100.0	364	6	ADA18786	Ada18786	Human	PRO
35	631	100.0	364	6	ADA61409	Ada61409	Homo sapi	
36	631	100.0	364	6	ADB19194	Adb19194	Novel	hum
37	631	100.0	364	6	ADB27735	Adb27735	Human	PRO
38	631	100.0	364	6	ADA86214	Ada86214	Novel	hum
39	631	100.0	364	6	ADB15778	Adb15778	Human	PRO
40	631	100.0	364	6	ADA47564	Ada47564	Human	PRO
41	631	100.0	364	6	ADA67359	Ada67359	Human	PRO
42	631	100.0	364	6	ADB30366	Adb30366	Human	PRO
43	631	100.0	364	6	ADA85662	Ada85662	Novel	hum
44	631	100.0	364	6	ADA96874	Ada96874	Human	PRO
45	631	100.0	364	6	ADA79178	Ada79178	Human	PRO
46	631	100.0	364	6	ADA87317	Ada87317	Novel	hum
47	631	100.0	364	6	ADB16519	Adb16519	Human	PRO
48	631	100.0	364	6	ADA91611	Ada91611	Novel	hum
49	631	100.0	364	6	ADB14674	Adb14674	Human	PRO
50	631	100.0	364	6	ADB18635	Adb18635	Novel	hum
51	631	100.0	364	6	ADA93850	Ada93850	Human	PRO
52	631	100.0	364	6	ADB19746	Adb19746	Novel	hum
53	631	100.0	364	6	ADB13058	Adb13058	Human	PRO
54	631	100.0	364	6	ABO43241	Abu43241	Novel	hum
55	631	100.0	364	6	ADA74312	Ada74312	Human	PRO
56	631	100.0	364	6	ADB24545	Adb24545	Human	PRO
57	631	100.0	364	6	ADA82069	Ada82069	Human	PRO
58	631	100.0	364	6	ADA75032	Ada75032	Human	PRO
59	631	100.0	364	6	ADA85110	Ada85110	Novel	hum
60	631	100.0	364	6	ADA84558	Ada84558	Novel	hum
61	631	100.0	364	6	ADB29814	Adb29814	Human	PRO
62	631	100.0	364	6	ADA80342	Ada80342	Human	PRO
63	631	100.0	364	6	ADA75584	Ada75584	Human	PRO
64	631	100.0	364	6	ADA46809	Ada46809	Human	PRO
65	631	100.0	364	6	ADB25105	Adb25105	Human	PRO
66	631	100.0	364	6	ADA93281	Ada93281	Human	PRO
67	631	100.0	364	6	ADB26631	Adb26631	Human	PRO
68	631	100.0	364	6	ADB30918	Adb30918	Human	PRO
69	631	100.0	364	6	ADA60846	Ada60846	Homo sapi	
70	631	100.0	364	6	ADB23993	Adb23993	Human	PRO
71	631	100.0	364	6	ADA96322	Ada96322	Human	PRO
72	631	100.0	364	6	ADA80894	Ada80894	Human	PRO
73	631	100.0	364	6	ADA95770	Ada95770	Human	PRO
74	631	100.0	364	6	ADB26079	Adb26079	Human	PRO
75	631	100.0	364	6	ADB21564	Adb21564	Novel	hum
76	631	100.0	364	7	ADA77343	Ada77343	Human	PRO
77	631	100.0	364	7	ADB18083	Adb18083	Human	PRO
78	631	100.0	364	7	ADA86766	Ada86766	Novel	hum
79	631	100.0	364	7	ADA87869	Ada87869	Novel	hum
80	631	100.0	364	7	ADA46257	Ada46257	Novel	hum
81	631	100.0	364	7	ADB28287	Adb28287	Human	PRO
82	631	100.0	364	7	ADB28839	Adb28839	Human	PRO
83	631	100.0	364	7	ADA76791	Ada76791	Human	PRO
84	631	100.0	364	7	ADA88421	Ada88421	Novel	hum
85	631	100.0	364	7	ADA97426	Ada97426	Human	PRO
86	631	100.0	364	7	ADB27183	Adb27183	Human	PRO
87	631	100.0	364	7	ADB22116	Adb22116	Novel	hum
88	631	100.0	364	7	ADA66807	Ada66807	Human	PRO
89	631	100.0	364	7	ADB22668	Adb22668	Human	PRO
90	631	100.0	364	7	ADB23441	Adb23441	Human	PRO
91	631	100.0	364	7	ADA92163	Ada92163	Novel	hum
92	631	100.0	364	7	ADB15226	Adb15226	Human	PRO
93	631	100.0	364	7	ADB38478	Adb38478	Novel	hum
94	631	100.0	364	7	ADB37926	Adb37926	Novel	hum
95	631	100.0	364	7	ADB66398	Adb66398	Novel	hum
96	631	100.0	364	7	ADB89478	Adb89478	Human	PRO
97	631	100.0	364	7	ADB90210	Adb90210	Human	PRO
98	631	100.0	364	7	ADB39311	Adb39311	Novel	hum

99 631 100.0 364 7 ADB46934 Novel hum
100 631 100.0 364 7 ADB86541 Human PRO

ALIGNMENTS

RESULT 1
ADK68116
ID ADK68116 standard; protein; 123 AA.
XX
AC ADK68116;
XX
DT 06-MAY-2004 (first entry)
XX
DE Novel NOVX protein #21.
XX
KW anti-diabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW antiarthritic; antiinflammatory; dermatological; antiasthmatic;
KW antileptic; gene therapy; metabolic disorder; diabetes; obesity;
KW infectious disease; anorexia; cancer; cardiovascular disease;
KW hypertension; atherosclerosis; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW asthma; dyslipidemia; neurogenesis; cell differentiation;
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; pharmacogenomic.
XX
OS Homo sapiens.
XX
PN WO2003085124-A2.
XX
PD 16-OCT-2003.
XX
PF 01-APR-2003; 2003WO-US009775.
XX
PR 01-APR-2002; 2002US-0369065P.
PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsbrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL;
PI Grosse WM, Gunther E, Guev VY, Heyes MP, Lepley DM, Li L;
PI Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shinkets RD, Smithson G, Stone DJ;
PI Vernet CAM, Voss EZ;
XX
XX WPI; 2003-812730/76.
XX N-PSDB; ADK68115.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
XX preventing, diagnosing or treating NOVX-associated disorders, e.g.
XX osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
XX asthma, or infections.
XX
XX Claim 1; SEQ ID NO 42; 323pp; English.
XX
XX The invention relates to novel NOVX protein and their encoding DNA's,
XX mature forms of the proteins or sequences that are at least 95% identical

CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.
XX
SQ Sequence 123 AA;
Query Match 100.0%; Score 631; DB 7; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.2e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDLRLNDADKRYSCYTPRNYSVNIRELKLAVVFFPRCLLVQRCCGCGTVNWRSC 60
Db 11 VDLRLNDADKRYSCYTPRNYSVNIRELKLAVVFFPRCLLVQRCCGCGTVNWRSC 70
Qy 61 CNSGKTVKKYHEVLOPEPGHIKRRGAKTVALVDIQLDHHRCDCICSSRPPR 113
Db 71 CNSGKTVKKYHEVLOPEPGHIKRRGAKTVALVDIQLDHHRCDCICSSRPPR 123
RESULT 2
ADK49105
ID ADK49105 standard; protein; 123 AA.
XX
AC ADK49105;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human NOV4c protein.
XX
KW NOVX; human; cardiomyopathy; atherosclerosis; hypertension,
KW pulmonary stenosis; obesity; prostate cancer; diabetes; haemophilia;
KW skin disorder; graft versus host disease; AIDS; asthma; lupus;
KW Crohn's disease; inflammatory bowel disease; ulcerative colitis;
KW multiple sclerosis; infectious disease; anorexia; Alzheimer's disease;
KW Parkinson's disease; NOV4c.
XX
OS Homo sapiens.
XX
XX US2004162236-A1.
PN
XX
XX 19-AUG-2004.
PD
XX
XX 31-MAR-2003; 2003US-00403142.
XX
XX
PR 01-APR-2002; 2002US-0369065P.
PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 05-APR-2002; 2002US-0370381P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.

PR 15-AUG-2002; 2002US-0403748P.
XX (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASN/) CASHAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALV/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
XX
XX Alsobrook J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC;
PI Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E;
PI Gusev V, Heyes M, Lepley D, Li L, MacDougall JR, Malyankar UM;
PI Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S;
PI Shimkets R, Smithson G, Stone D, Vernet C, Voss E;
XX
XX WPI; 2004-603580/58.
DR N-PSDB; ADR49104.
XX
XX New isolated polypeptides and nucleic acids, useful for treating or
PT preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity,
PT prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease,
PT or infectious disease.
XX
XX Claim 1; SEQ ID NO 42; 206pp; English.
XX
XX This invention describes novel human NOVX polypeptides and the
CC polynucleotides encoding them. The therapeutic is useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease selected from pathology associated with the polypeptide.
CC Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary
CC stenosis, obesity, prostate cancer, diabetes, hemophilia, skin
CC disorders, graft versus host disease, AIDS, asthma, lupus, Crohn's
CC disease, inflammatory bowel disease, ulcerative colitis, multiple
CC sclerosis, infectious disease, anorexia, Alzheimer's disease, or
CC Parkinson's disease. They are also useful in detection assays, chromosome
CC mapping, or tissue typing. This sequence represents the human NOV4C
XX protein.
XX
SQ Sequence 123 AA;
Query Match 100.0%; Score 631; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.2e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLDRLNDKAYSCPTPNYSVNIREEKLKLVVFPFRCCLLVQRCGCGCGTNNRST 60
DB 11 VLDRLNDKAYSCPTPNYSVNIREEKLKLVVFPFRCCLLVQRCGCGCGTNNRST 70
QY 61 CNSGKTVKKYHEVLQPEPGHIKRRGAKTMALVDIOLDHHERCDCICSSRPPR 113
|||||

Db 71 CNSGKTVKKYHEVLQPEPGHIKRRGAKTMALVDIOLDHHERCDCICSSRPPR 123
RESULT 3
AAU00699
ID AAU00699 standard; protein; 132 AA.
XX AC AAU00699;
XX 07-SEP-2001 (first entry)
XX Human FCTR2 protein present in clone 30664188.0.331.
XX
XX Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
KW inflammatory disorder; graft versus host disease; coagulation;
KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
KW peripheral neuropathy; acute brain injury.
XX
XX Homo sapiens.
XX
XX WO200125437-A2.
XX PD 12-APR-2001. possible
XX PF 06-OCT-2000; 2000WO-US027671.
XX
XX 07-OCT-1999; 99US-0158083P.
PR 13-OCT-1999; 99US-0159231P.
PR 04-JAN-2000; 2000US-0174485P.
PR 03-MAR-2000; 2000US-0186707P.
PR 10-MAR-2000; 2000US-0189250P.
PR 08-AUG-2000; 2000US-0223879P.
PR 12-SEP-2000; 2000US-00662783.
PR 20-SEP-2000; 2000US-0234082P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX
XX WPI; 2001-316172/33.
DR N-PSDB; AAS04493.
XX
XX Novel growth factor polypeptides termed as FCTR polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
XX Claim 1; Page 14-15; 171pp; English.
XX
XX The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
CC FCTR proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the protein in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting
CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, Graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy


```
RESULT 6
ADK68112
ID ADK68112 standard; protein; 132 AA.
XX
AC ADK68112;
XX
DT 06-MAY-2004 (first entry)
XX
DE Novel NOVX protein #19.
XX
KW antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW antarthritic; antiinflammatory; dermatological; antiasthmatic;
KW antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW infectious disease; anorexia; cancer; cardiovascular disease;
KW hypertension; atherosclerosis; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW asthma; dyalipidemia; neurogenesis; cell differentiation;
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; pharmacogenomic.
XX
OS Homo sapiens.
XX
PN WO2003085124-A2.
XX
PD 16-OCT-2003.
XX
PF 01-APR-2003; 2003WO-US0099775.
XX
PR 01-APR-2002; 2002US-0369065P.
PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL;
PI Grose WM, Gunther E, Gusev VV, Heyes MP, Lepley DM, Li L;
PI Macdougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shinkets RD, Smithson G, Stone DJ;
PI Vernet CAM, Voss EZ;
XX
WPI; 2003-812730/76.
DR N-PSDB; ADK68111.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; SEQ ID NO 38; 323pp; English.
XX
CC The invention relates to novel NOVX protein and their encoding DNA's,
CC mature forms of the proteins or sequences that are at least 95% identical
CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such metabolic disorders,
```

```
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.
```

Sequence 132 AA;

Query Match 100.0%; Score 631; DB 7; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.5e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLDRLNDDAKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGNGCGGTVNRSC 60

DB 20 VLDRLNDDAKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGNGCGGTVNRSC 79

QY 61 CNSGKTVKKYHEVLQFEPGHKKRGRKTMALVDIQLDHHRCDCICSSRP 113

DB 80 CNSGKTVKKYHEVLQFEPGHKKRGRKTMALVDIQLDHHRCDCICSSRP 132

RESULT 7

ADM57645

ID ADM57645 standard; protein; 132 AA.

XX

AC ADM57645;

XX DT 03-JUN-2004 (first entry)

XX DE Human FCTR2 protein.

XX KW Fibroblast growth factor-CX; FGF-CX; FCTR; inflammatory bowel disease;
XX KW inflammation; Crohn's disease; gene therapy;
XX KW platelet-derived growth factor; PDGFB; human.

XX OS Homo sapiens.

XX PN US2004006015-A1.

XX PD 08-JAN-2004.

XX PF 16-DEC-2002; 2002US-00321962.

XX PR 16-NOV-2001; 2001US-00011364.

XX PR 06-JUN-2002; 2002US-0386545P.

XX PA (BOLD/) BOLDOG F L.

XX PA (BURG/) BURGESS C E.

XX PA (FERN/) FERNANDES E R.

XX PA (JEFF/) JEFFERS M E.

XX PA (LARO/) LAROCHELLE W J.

XX PA (LICH/) LICHENSTEIN H S.

XX PA (PETE/) PETERSON J.

XX PA (PRAY/) PRAYAGA S K.

XX PA (RITT/) RITTMAN B.

XX PA (SHIM/) SHIMKETS J B.

XX PA (SHIM/) SHIMKETS R A.

XX PA (YANG/) YANG M.

XX Boldog FL, Burgess CE, Fernandes ER, Jeffers ME, Larochelle WJ;

PI Lichenstein HS, Peterson J, Prayaga SK, Rittman B, Shinkets JB;

PI Shinkets RA, Yang M;

XX WPI; 2004-081737/08.

DR

DR N-PSDB; ADM57644.

XX Promoting the growth of a population of cells, useful for treating

PT inflammatory conditions, comprises contacting the at least one cell with

PT a composition comprising FGFCX and/or FCTR protein.

XX

PS Claim 4; SEQ ID NO 6; 153pp; English.

XX

CC The present invention is based upon methods of treating inflammatory

CC conditions in the intestinal tract of mammals using fibroblast growth

CC factor (FGF)-CX and/or FCTR (undefined) polypeptides and their encoding

CC polynucleotides. The invention is useful for treating inflammatory

CC pathology such as inflammatory bowel disease, inflammatory condition

CC occurring in the colon or small intestine and Crohn's disease. The

CC invention is also useful in gene therapy. The present sequence is human

CC FCTR protein. The sequence is also referred as human platelet-derived

CC growth factor D (PDGFD) protein.

XX

SQ Sequence 132 AA;

Query Match 100.0%; Score 631; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 3.5e-62;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTNNRSCT 60

DB 20 VDLRLNDADKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTNNRSCT 79

QY 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113

DB 80 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 132

RESULT 8

ADR49101

ID ADR49101 standard; protein; 132 AA.

XX

AC ADR49101;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human NOV4a protein.

XX

KW NOVX; human; cardiomyopathy; atherosclerosis; hypertension;

KW pulmonary stenosis; obesity; prostate cancer; diabetes; haemophilia;

KW skin disorder; graft versus host disease; AIDS; asthma; lupus;

KW Crohn's disease; inflammatory bowel disease; ulcerative colitis;

KW multiple sclerosis; infectious disease; anorexia; Alzheimer's disease;

KW Parkinson's disease; NOV4a.

XX

OS Homo sapiens.

XX

FN US2004162236-A1.

XX

PD 19-AUG-2004.

XX

PF 31-MAR-2003; 2003US-00403142.

XX

PR 01-APR-2002; 2002US-0369065P.

PR 05-APR-2002; 2002US-0370279P.

PR 05-APR-2002; 2002US-0370359P.

PR 08-APR-2002; 2002US-0370381P.

PR 08-APR-2002; 2002US-0370969P.

PR 12-APR-2002; 2002US-0372019P.

PR 22-APR-2002; 2002US-0374379P.

PR 15-MAY-2002; 2002US-0380973P.

PR 30-MAY-2002; 2002US-0384297P.

PR 30-MAY-2002; 2002US-0384329P.

PR 17-JUN-2002; 2002US-0389729P.

PR 13-AUG-2002; 2002US-0403491P.

PR 15-AUG-2002; 2002US-0403748P.

XX

PA (ALSO/) ALSOBROOK J.

PA (BENT/) BENTO P.

PA (BOLD/) BOLDOG F.

PA (BURG/) BURGESS C.

PA (CASW/) CASMAN S.

PA (BOKO/) BOKOR J C.

PA (EDIN/) EDINGER S R.

PA (ELLE/) ELLERMAN K.

PA (FERN/) FERNANDES E.

PA (GERL/) GERLACH V.

PA (GROS/) GROSSE W.

PA (GUNT/) GUNTHER E.

PA (GUSE/) GUSEV V.

PA (HEVE/) HEYES M.

PA (LEPL/) LEPLEY D.

PA (LILL/) LI L.

PA (MACD/) MACDOUGALL J R.

PA (MALY/) MALYANKAR U M.

PA (MILL/) MILLET I.

PA (PATT/) PATTURAJAN M.

PA (PEYM/) PEYMAN J A.

PA (RAST/) RASTELLI L.

PA (RIEG/) RIEGER D.

PA (SHEN/) SHENOY S.

PA (SHIM/) SHIMKETS R.

PA (SMIT/) SMITHSON G.

PA (STON/) STONE D.

PA (VERN/) VERNET C.

PA (VOSS/) VOSS E.

XX

PI Alsbrook J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC;

PI Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E;

PI Gusev V, Heyes M, Lepley D, Li L, Macdougall JR, Malyankar UM;

PI Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S;

PI Shimkets R, Smithson G, Stone D, Vernet C, Voss E;

XX

DR WPI; 2004-603580/58.

DR N-PSDB; ADR49100.

XX

PT New isolated polypeptides and nucleic acids, useful for treating or

PT preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity,

PT prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease,

PT or infectious disease.

XX

PS Claim 1; SEQ ID NO 38; 206pp; English.

XX

CC This invention describes novel human NOVX polypeptides and the

CC polynucleotides encoding them. The therapeutic is useful in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease selected from pathology associated with the polypeptide.

CC Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary

CC stenosis, obesity, prostate cancer, diabetes, haemophilia, skin

CC disorders, graft versus host disease, AIDS, asthma, lupus, Crohn's

CC disease, inflammatory bowel disease, ulcerative colitis, multiple

CC sclerosis, infectious disease, anorexia, Alzheimer's disease, or

CC Parkinson's disease. They are also useful in detection assays, chromosome

CC mapping, or tissue typing. This sequence represents the human NOV4a

CC protein.

XX

SQ Sequence 132 AA;

Query Match 100.0%; Score 631; DB 8; Length 132;

Best Local Similarity 100.0%; Pred. No. 3.5e-62;

Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTNNRSCT 60

DB 20 VDLRLNDADKRYCTPRNYSWNIREELKLANVFFPRCLLVQRCGCGGTNNRSCT 79

QY 61 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113

DB 80 CNSGKTVKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 132

RESULT 9
 ABB11697
 ID ABB11697 standard; peptide; 152 AA.
 XX
 AC ABB11697;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human novel protein, SEQ ID NO:2067.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001. *W05:0 bcl*
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457740/49.
 DR N-PSDB; ABA08941.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 229; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 SQ Sequence 152 AA;
 XX
 Query Match 100.0%; Score 631; DB 4; Length 152;
 Best Local Similarity 100.0%; Pred. No. 4.1e-62;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 VDLRLNDADAKYSGCTPRNYSVINREELKLANVFFPRCLLVQRCGNGCGCTVNRSGT 60
 Db 40 VDLRLNDADAKYSGCTPRNYSVINREELKLANVFFPRCLLVQRCGNGCGCTVNRSGT 99
 QY 61 CNSGKTVKYYHEVLFQEPGHKRRGRAKTMALVDIQLDHHRCDCICSSRPR 113
 Db 100 CNSGKTVKYYHEVLFQEPGHKRRGRAKTMALVDIQLDHHRCDCICSSRPR 152
 XX
 RESULT 10
 AAU00702
 ID AAU00702 standard; protein; 154 AA.
 XX
 AC AAU00702;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human FCTR5 protein present in clone pCR2.1-S852_2B.
 XX
 KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
 KW VEGF-E; platelet derived growth factor; PDGF; hyperplasia; cancer;
 KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
 KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
 KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
 KW inflammatory disorder; Graft versus host disease; coagulation;
 KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
 KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
 KW peripheral neuropathy; acute brain injury.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein /note= "Signal peptide"
 FT 24..154
 FT /note= "Mature FCTR5"
 XX
 WO200125437-A2.
 PD 12-APR-2001. *W05:0 bcl*
 XX
 PF 06-OCT-2000; 2000WO-US027671.
 XX
 PR 07-OCT-1999; 99US-0158083P.
 PR 13-OCT-1999; 99US-0159231P.
 PR 04-JAN-2000; 2000US-0174485P.
 PR 03-MAR-2000; 2000US-0186707P.
 PR 10-MAR-2000; 2000US-0188250P.
 PR 08-AUG-2000; 2000US-0223879P.
 PR 12-SEP-2000; 2000US-00662783.
 PR 20-SEP-2000; 2000US-0234082P.
 XX
 PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX
DR WPI; 2001-316172/33.
DR N-PSDB; AAS04496.
XX
XX Novel growth factor polypeptides termed as FCTR5 polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
XX
PS Claim 1; Page 19; 171pp; English.
XX
XX The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR5 peptides and nucleic acids.
CC FCTR5 proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the proteins in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting
CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy
XX
SQ Sequence 154 AA;
Query Match 100.0%; Score 631; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.1e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDADKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGCGGTVNRSC 60
DB 42 VDLRLNDADKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGCGGTVNRSC 101
QY 61 CNSGKTVKXHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPP 113
DB 102 CNSGKTVKXHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPP 154
RESULT 11
ABB79647
ID ABB79647 standard; protein; 154 AA.
AC ABB79647;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human FCTR5 (platelet derived growth factor D).
XX
XX FCTR5; platelet derived growth factor D; PDGFD; human; Crohn's disease;
KW inflammatory bowel disease; gene therapy; antiinflammatory; vulnerary;
KW cystostatic; cardiovascular.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Key 1..23
FT Peptide /label= Signal_peptide
FT Protein 24..154
FT /label= Mature_protein
XX
XX WO200258716-A2.
PN
XX
XX 01-AUG-2002.
XX

PF 06-NOV-2001; 2001WO-US043846.
XX
PR 06-NOV-2000; 2000US-0246206P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Jeffers M, Shimkets RA, Pravaga S, Boldog FL, Yang M, Burgess CE;
PI Fernandes ER, Rittman B, Shimkets JB, Larochele WJ, Lichenstein HS;
XX
DR WPI; 2002-599742/64.
DR N-PSDB; ABB84528.
XX
XX Treating, delaying the onset of, or ameliorating an inflammatory
PT pathology (e.g. inflammatory bowel disease or Crohn's disease) by
PT administering to the subject fibroblast growth factors or a combination
PT of growth factors.
XX
PS Claim 5; Page 26; 196pp; English.
XX
XX The present sequence is the protein sequence of FCTR5, also referred to
CC as platelet derived growth factor D (PDGFD) or human PDGFD. FCTR5 is a
CC splice variant of FCTR1 (see ABB79643). It contains a characteristic
CC signal peptide, PDGF domain and N-glycosylation site. Human FCTR5 is most
CC closely related to human PDGF C, B and A. The invention provides FPCR5
CC and FCTR5 growth factors, polypeptides and variants, and polynucleotides
CC encoding them, and methods of using these to treat, delay the onset of,
CC or ameliorate, an inflammatory pathology, especially inflammatory bowel
CC disease, a disease that occurs in the colon or small intestine, or
CC Crohn's disease (all claimed). The FPCR5 and FCTR5 polypeptides and
CC polynucleotides are also useful for treating growth and proliferative
CC diseases such as cancer, angiogenesis, collagen formation, fibrotic and
CC cardiovascular diseases or diabetic ulcers, and in wound healing. They
CC can be used in screening and detection methods, chromosome mapping,
CC tissue typing, predictive medicine, diagnostic assays, prognostic assays,
CC and pharmacogenomics
XX
SQ Sequence 154 AA;
Query Match 100.0%; Score 631; DB 5; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.1e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDADKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGCGGTVNRSC 60
DB 42 VDLRLNDADKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGCGGTVNRSC 101
QY 61 CNSGKTVKXHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPP 113
DB 102 CNSGKTVKXHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPP 154
RESULT 12
ADM57651
ID ADM57651 standard; protein; 154 AA.
XX
XX ADM57651;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human FCTR5 protein.
XX
XX Fibroblast growth factor-CX; FGF-CX; FCTR5; inflammatory bowel disease;
KW inflammation; Crohn's disease; gene therapy;
KW platelet-derived growth factor; PDGFD; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Key 1..23
FT Peptide /label= Signal_peptide
FT Protein 24..154
FT /note= "Human mature FCTR5 protein"
XX

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PN US2004006015-A1.
XX
PD 09-JAN-2004.
XX
PF 16-DEC-2002; 2002US-00321962.
XX
PR 16-NOV-2001; 2001US-00011364.
XX
PR 06-JUN-2002; 2002US-0386545P.
XX
(BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (FERN/) FERNANDES E R. I
PA (JEFF/) JEFFERS M E.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (PETE/) PETERSON J.
PA (PRAY/) PRAYAGA S K.
PA (RITT/) RITTMAN B.
PA (SHIM/) SHIMKETS J B.
PA (SHIM/) SHIMKETS R A.
PA (YANG/) YANG M.
XX
XX Boldog FL, Burgess CE, Fernandes ER, Jeffers ME, Larochelle WJ;
PI Lichenstein HS, Peterson J, Prayaga SK, Rittman B, Shimkets JB;
PI Shimkets RA, Yang M;
XX
XX WPI; 2004-081737/08.
DR N-PSDB; ADM57650.
XX
XX Promoting the growth of a population of cells, useful for treating
PT inflammatory conditions, comprises contacting the at least one cell with
PT a composition comprising FGFX and/or FCTX polypeptides.
XX
XX Claim 4; SEQ ID NO 12; 153pp; English.
XX
XX The present invention is based upon methods of treating inflammatory
CC conditions in the intestinal tract of mammals using fibroblast growth
CC factor (FGF)-CX and/or FCTX(undefined) polypeptides and their encoding
CC polynucleotides. The invention is useful for treating inflammatory
CC pathology such as inflammatory bowel disease, inflammatory condition
CC occurring in the colon or small intestine and Crohn's disease. The
CC invention is also useful in gene therapy. The present sequence is human
CC FCTX protein. The sequence is also referred as human platelet-derived
CC growth factor D (PDGFD) cDNA.
XX
XX Sequence 154 AA;
SQ
Query Match 100.0%; Score 631; DB 8; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.1e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDADAKYSCYCTPRNYSVNIREELKLVNVPFRCCLLVQRCGNGCGGTNNRSCT 60
DB 42 VDLRLNDADAKYSCYCTPRNYSVNIREELKLVNVPFRCCLLVQRCGNGCGGTNNRSCT 101
QY 61 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 113
DB 102 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 154
RESULT 13
ABU72441
ID ABU72441 standard; protein; 302 AA.
XX
XX ABU72441;
AC
XX 16-JUN-2003 (first entry)
DT
XX ZVEGF4-related fusion protein #1.
DE
XX Growth factor homologue; ZVEGF4; proliferation; differentiation;
KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW neurite growth; cardiovascular development; limb development;
```

```
KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
KW autoimmune disease; inflammation; retinopathy; haemangioma;
KW ischaemic event; neuropathy; acute nerve damage; stroke;
KW central nervous system disease; peripheral nervous system disease.
XX
OS Unidentified.
XX
XX US6495668-B1.
XX
XX 17-DEC-2002.
XX
XX 03-MAY-2000; 2000US-00564595.
XX
XX 03-MAY-1999; 99US-0132250P.
XX 10-NOV-1999; 99US-016463P.
XX 04-FEB-2000; 2000US-0180169P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI WPI; 2003-352153/33.
XX
XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.
XX
XX Claim 14; Col 107-110; 67pp; English.
XX
XX The invention relates to an isolated protein comprising a first
CC polypeptide disulphide-bonded to a second polypeptide. The first and
CC second polypeptides are from 113-138 amino acid residues and comprises
CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
CC protein stimulates proliferation, differentiation, or migration of
CC mesenchymal cells and may modulate activities mediated by cell surface
CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
CC semaphorin interactions which may be of use in neurite growth,
CC cardiovascular development, cartilage and limb development, T- and B-cell
CC functions as well as treating rheumatoid arthritis, various forms of
CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
CC ischaemic events, neuropathies, acute nerve damage, central nervous
CC system diseases and peripheral nervous system diseases including stroke.
CC The isolated protein is also used for a pharmaceutical composition as
CC therapeutic agents, diagnostic agents, and research tools and reagents.
CC It can be used in the study and regulation of cell and tissue
CC development, as components of cell culture media. The proteins can form
CC homodimers or heterodimers that act on tissues to control organ
CC development by modulating cell proliferation, migration, differentiation,
CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
CC -23.1. The present sequence represents a ZVEGF4-related fusion protein
CC (claimed but not further defined in the specification)
XX
XX Sequence 302 AA;
SQ
Query Match 100.0%; Score 631; DB 6; Length 302;
Best Local Similarity 100.0%; Pred. No. 8.8e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDADAKYSCYCTPRNYSVNIREELKLVNVPFRCCLLVQRCGNGCGGTNNRSCT 60
DB 190 VDLRLNDADAKYSCYCTPRNYSVNIREELKLVNVPFRCCLLVQRCGNGCGGTNNRSCT 249
QY 61 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 113
DB 250 CNSGKTVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPPR 302
RESULT 14
ADJ32807
ID ADJ32807 standard; protein; 302 AA.
XX
XX ADJ32807;
AC
```

DT 15-APR-2004 (first entry)
DE Fusion protein #1 used in the invention.
XX
XX Growth factor homologue; zvegfg4; skin wound; venous stasis; ulcer;
KW fracture repair; skin grafting; neovascularisation;
KW female reproductive tract disorder; bleeding; gastrointestinal tract;
KW liver damage; hepatic chronic passive congestion; CPC;
KW central haemorrhagic necrosis; CHN; neurite growth; neuropathy;
KW neurodegenerative disease; multiple sclerosis; Alzheimer's disease;
KW Parkinson's disease; cell proliferation; cancer; gene therapy.
XX
XX Unidentified.
OS
XX
XX US2004002140-A1.
PN
XX
XX 01-JAN-2004.
PD
XX
XX 06-JUN-2001; 2001US-00876813.
PF
XX
XX 03-MAY-1999; 99US-0132250P.
PR
XX
XX 10-NOV-1999; 99US-0164463P.
PR
XX
XX 04-FEB-2000; 2000US-0180169P.
PR
XX
XX 03-MAY-2000; 2000US-00564595.
XX
XX (GILB/) GILBERT T.
PA (HART/) HART C.E.
PA (SHEP/) SHEPPARD P.O.
PA (GILB/) GILBERTSON D.G.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
XX
XX WPI; 2004-070738/07.
DR
XX
XX New zvegfg4 polypeptides and nucleic acids, useful for diagnosing or
PT treating cell loss or abnormal cell proliferation, e.g. cancer, treating
PT full-thickness skin wounds or treating female reproductive tract
PT disorders.
XX
XX Disclosure; SEQ ID NO 54; 73pp; English.
XX
XX The invention relates to growth factor homologue zvegfg4, its
CC corresponding nucleic acid and methods of using them. The sequences of
CC the invention are used in the study and regulation of cell and tissue
CC development, as components of cell culture media and as diagnostic
CC agents. The zvegfg4 polypeptide can be used in treating full-thickness
CC skin wounds, including venous stasis, ulcers and other chronic, non-
CC healing wounds, in fracture repair, skin grafting, in constructive
CC surgery to promote neovascularisation and increase skin flap survival, to
CC establish vascular networks in transplanted cells and tissues, or in
CC treating female reproductive tract disorders, including acute or chronic
CC placental insufficiency and prolonged bleeding. It can also be used to
CC promote endothelialisation of vascular grafts and stents, in treating
CC acute or chronic lesions of the gastrointestinal tract or treating or
CC repairing liver damage. Zvegfg4 can also be used for treating hepatic
CC chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN).
CC Zvegfg4 proteins, agonists and antagonists can also be used to modulate
CC neurite growth and development and demarcate nervous system structures.
CC It can also be used for treating peripheral neuropathies or
CC neurodegenerative diseases including multiple sclerosis, Alzheimer's
CC disease or Parkinson's disease. The polypeptides, nucleic acids and
CC antibodies can also be used to diagnose or treat disorders associated
CC with cell loss or abnormal cell proliferation (including cancer). The
CC invention is useful in gene therapy. The present sequence is a fusion
CC protein used in the invention.
XX
XX Sequence 302 AA;
SQ
Query Match 100.0%; Score 631; DB 8; Length 302;
Best Local Similarity 100.0%; Pred. No. 8.8e-62;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 VDLRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRLCLLVQRCGCGCTVNRSGT 60

Db 190 VDLRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRLCLLVQRCGCGCTVNRSGT 249
Qy 61 CNSGKTWKYKHYEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPR 113
Db 250 CNSGKTWKYKHYEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPR 302
RESULT 15
ABU72442
ID ABU72442 standard; protein; 316 AA.
XX
XX AC ABU72442;
XX
XX DT 16-JUN-2003 (first entry)
XX
XX DE ZVEGF4-related fusion protein #2.
XX
XX KW Growth factor homologue; ZVEGF4; proliferation; differentiation;
KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW neurite growth; cardiovascular development; limb development;
KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
KW autoimmune disease; inflammation; retinopathy; haemangioma;
KW ischaemic event; neuropathy; acute nerve damage; stroke;
KW central nervous system disease; peripheral nervous system disease.
XX
XX OS Unidentified.
XX
XX FN US6495668-B1.
XX
XX PD 17-DEC-2002.
XX
XX PF 03-MAY-2000; 2000US-00564595.
XX
XX PR 03-MAY-1999; 99US-0132250P.
PR 10-NOV-1999; 99US-0164463P.
PR 04-FEB-2000; 2000US-0180169P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
FI
XX
XX WPI; 2003-352153/33.
DR
XX
XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.
XX
XX Claim 14; Col 109-112; 67pp; English.
XX
XX The invention relates to an isolated protein comprising a first
CC polypeptide disulphide-bonded to a second polypeptide. The first and
CC second polypeptides are from 113-138 amino acid residues and comprises
CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
CC protein stimulates proliferation, differentiation, or migration of
CC mesenchymal cells and may modulate activities mediated by cell surface
CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
CC semaphorin interactions which may be of use in neurite growth,
CC cardiovascular development, cartilage and limb development, T- and B-cell
CC functions as well as treating rheumatoid arthritis, various forms of
CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
CC ischaemic events, neuropathies, acute nerve damage, central nervous
CC system diseases and peripheral nervous system diseases including stroke.
CC The isolated protein is also used for a pharmaceutical composition as
CC therapeutic agents, diagnostic agents, and research tools and reagents.
CC It can be used in the study and regulation of cell and tissue
CC development, as components of cell culture media. The proteins can form
CC homomultimers or heteromultimers that act on tissues to control organ
CC development by modulating cell proliferation, migration, differentiation,
CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
CC -23.1. The present sequence represents a ZVEGF4-related fusion protein
CC (claimed but not further defined in the specification)
XX

[illegible]

Secreted cellular growth factors are molecules which bind to cell surface receptors to regulate a variety of cellular pathways. Growth factors are important in signalling pathways related to embryonic patterning events, cell cycle control, apoptosis, cellular differentiation, cell motility and gene expression. Also disclosed are methods for identifying CC modulators or receptors of the growth factor and diagnosing a pathogenic CC condition, or susceptibility to a pathogenic condition, that is CC associated with a genetic alteration in the growth factor. The growth factor polynucleotide is useful for diagnosing, prognosing or treating (e.g. gene therapy) disorders that are associated with dysfunction of the CC growth factors, such as developmental and growth disorders, CC cardiovascular disorders, neurological disorders, metabolic disorders, cancer or immunological diseases. In particular, the polynucleotide is useful for treating or diagnosing e.g. diabetes, osteoporosis, CC hypercalcaemia or hyperparathyroid. The polynucleotide or polypeptide is also useful in drug screening, particularly for identifying modulators or CC receptors of growth factors. The sequence presented is the human growth factor, A.ccg12831-000000.10.0, which is disclosed as being encoded by CC the DNA presented in ABX11387

XX Sequence 317 AA:
SQ

Query Match	100.0%;	Score 631;	DB 6;	Length 317;
Best Local Similarity	100.0%;	Pred. No. 9.3e-62;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	V D L R L N D D A K R Y S C T P R N Y S V N I R E E L K L A N V V F P P R C L L V Q R C G N C G C G T V N W R S C T	60	
Db	205	V D L R L N D D A K R Y S C T P R N Y S V N I R E E L K L A N V V F P P R C L L V Q R C G N C G C G T V N W R S C T	264	
Qy	61	C N S G K T V K K Y H E V L O F P G H I K R R G R A K T M A L V I O L D H H E R C D C I C S S R P P R	113	
Db	265	C N S G K T V K K Y H E V L O F P G H I K R R G R A K T M A L V I O L D H H E R C D C I C S S R P P R	317	

RESULT 18	
AAAY71129	
ID	AAAY71129 standard; peptide; 322 AA.
XX	
AC	AAAY71129;
XX	
DT	08-SEP-2000 (first entry)
XX	
DE	Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.
XX	
KW	Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; tumour;
KW	VGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW	proliferative; activator; proliferation; differentiation; motility;
KW	growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW	atherosclerosis; wound; metastasis.
XX	
OS	Homo sapiens.
XX	
PN	WO200027879-A1.
XX	
PD	18-MAY-2000
XX	
PF	10-NOV-1999; 99WO-US026462.
XX	
PR	10-NOV-1998; 98US-0107852P.
PR	28-DEC-1998; 98US-0113997P.
PR	26-AUG-1999; 99US-0150604P.
PR	04-OCT-1999; 99US-0157108P.
PR	05-OCT-1999; 99US-0157756P.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX	
PI	Eriksson U, Aase K, Ponten A, Lee X, Tutela M, Alitalo K;
PI	Oostman A, Heidin C;
XX	
DR	WPI; 2000-376495/32.
DR	N-PSDB; AAD00737.

XX Novel polynucleotides encoding a novel growth factor of cells expressing
PT a platelet-derived growth factor, useful for diagnostic and therapeutic
PT applications, e.g. concerning cancer.
XX
XX Claim 25; Fig 6; 111pp; English.
XX
XX The present sequence is an N-terminally truncated polypeptide of human
CC platelet derived growth factor (PDGF)-D, formally known as vascular
CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
CC lambda2gt10 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC as an activator of proliferation, differentiation, growth and motility of
CC cells, that express PDGF-D receptor. This sequence is useful for
CC inhibiting the growth of tumours, that express PDGF-D, expression of PDGF
CC -D and its proteolytic cleavage for generating an activated truncated
CC form is useful for regulating receptor binding specificity of PDGF-D.
CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells
XX
XX Sequence 322 AA;
SQ

Query Match	100.0%;	Score 631;	DB 3;	Length 322;
Best Local Similarity	100.0%;	Pred. NO. 9.5e-62;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	VDLRLNDDAKRYSCTPRNVSVNI	REELKLANVVFPPRCILLVQRCGNGCGGTVNR	SCT 60
Db	210	VDLRLNDDAKRYSCTPRNVSVNI	REELKLANVVFPPRCILLVQRCGNGCGGTVNR	SCT 269
Qy	61	CNSGKTVKKYVHEVLQEPGHI	KERGRAKTWMALVDIQLDHHERCDCI	CSSRPPR 113
Db	270	CNSGKTVKKYVHEVLQEPGHI	KERGRAKTWMALVDIQLDHHERCDCI	CSSRPPR 322

RESULT 19	
ADK68120	
ID	ADK68120 standard; protein; 347 AA.
XX	
AC	ADK68120;
XX	
DT	06-MAY-2004 (first entry)
XX	
XX	Novel NOVX protein #23.
XX	
KW	antidiabetic; anorectic; cardiact; hypotensive; antiarteriosclerotic;
KW	anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
KW	neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW	antiarthritic; antinflammatory; dermatological; anischematic;
KW	antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW	infectious disease; anorexia; cancer; cardiovascular disease;
KW	hypertension; atherosclerosis; neurodegenerative disorder;
KW	Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;
KW	osteoarthritis; hematopoietic disorders; inflammatory skin disorder;
KW	asthma; dyslipidemia; neurogenesis; cell differentiation;
KW	cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW	chromosome mapping; pharmacogenomic.
XX	
XX	Homo sapiens.
XX	
XX	WO2003085124-A2.
XX	
PD	16-OCT-2003.
XX	
XX	01-APR-2003; 2003WO-US009775.
XX	
XX	01-APR-2002; 2002US-0369065P.
PR	03-APR-2002; 2002US-0370279P.
PR	03-APR-2002; 2002US-0370359P.
PR	08-APR-2002; 2002US-0370969P.
PR	12-APR-2002; 2002US-0372019P.
PR	22-MAY-2002; 2002US-0374379P.
PR	15-MAY-2002; 2002US-0380973P.

PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
PR 31-MAR-2003; 2003US-00403142.
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Bento P, Boldog FL, Burgess CE, Casman S, Bokor JC;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes E, Gerlach VL;
PI Grosse WM, Gunther E, Gusev V, Heyes M, Lepley DM, Li L;
PI MacDougall JR, Malyankar UM, Millet I, Patturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shinkets R, Smithson G, Stone DJ;
PI Vernet CAM, Voss E;
XX
XX WPI; 2003-812730/76.
DR N-PSDB; ADK68119.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; SEQ ID NO 46; 333pp; English.
XX
XX The invention relates to novel NOVX protein and their encoding DNA's,
CC mature forms of the proteins or sequences that are at least 95% identical
CC to, or having one or more conservative amino acid substitutions in, the
CC proteins. The polypeptides, nucleic acid molecules and antibodies are
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
CC also be used as targets for the identification of small molecules that
CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX proteins of the invention.
XX
XX Sequence 347 AA;
SQ
Query Match 100.0%; Score 631; DB 7; Length 347;
Best Local Similarity 100.0%; Pred. No. 1e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLDRLLNDKAKYSCCTPRNYSVNIIRBELKLANVFPFRCLLVQRCGNCGGTNNRST 60
Db 235 VLDRLLNDKAKYSCCTPRNYSVNIIRBELKLANVFPFRCLLVQRCGNCGGTNNRST 294
QY 61 CNSGKTVKKYKHEVLQEPGHIKRGRAKTMALVDIQLDHHRCDCICSSRP 113
Db 295 CNSGKTVKKYKHEVLQEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRP 347
RESULT 20
ADR49109
ID ADR49109 standard; protein; 347 AA.
XX
XX ADR49109;
XX
XX 04-NOV-2004 (first entry)
XX Human NOV4e protein.

XX NOVX; human; cardiomyopathy; atherosclerosis; hypertension;
KW pulmonary stenosis; obesity; prostate cancer; diabetes; hemophilia;
KW skin disorder; graft versus host disease; AIDS; asthma; lupus;
KW Crohn's disease; inflammatory bowel disease; ulcerative colitis;
KW multiple sclerosis; infectious disease; anorexia; Alzheimer's disease;
KW Parkinson's disease; NOV4e.
XX
XX Homo sapiens.
XX
XX US2004162236-A1.
XX
XX 19-AUG-2004.
XX
XX 31-MAR-2003; 2003US-00403142.
XX
XX 01-APR-2002; 2002US-0169065P.
PR 05-APR-2002; 2002US-0370279P.
PR 05-APR-2002; 2002US-0370359P.
PR 05-APR-2002; 2002US-0370381P.
PR 08-APR-2002; 2002US-0370969P.
PR 12-APR-2002; 2002US-0372019P.
PR 22-APR-2002; 2002US-0374379P.
PR 15-MAY-2002; 2002US-0380973P.
PR 30-MAY-2002; 2002US-0384297P.
PR 30-MAY-2002; 2002US-0384329P.
PR 17-JUN-2002; 2002US-0389729P.
PR 13-AUG-2002; 2002US-0403491P.
PR 15-AUG-2002; 2002US-0403748P.
XX (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLER/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHINKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
XX
XX Alsobrook J, Bento P, Boldog F, Burgess C, Casman S, Bokor JC;
PI Edinger SR, Ellerman K, Fernandes E, Gerlach V, Grosse W, Gunther E;
PI Gusev V, Heyes M, Lepley D, Li L, MacDougall JR, Malyankar UM;
PI Millet I, Patturajan M, Peyman JA, Rastelli L, Rieger D, Shenoy S;
PI Shinkets R, Smithson G, Stone D, Vernet C, Voss E;
XX
XX WPI; 2004-603580/58.
DR N-PSDB; ADR49108.
XX
XX New isolated polypeptides and nucleic acids, useful for treating or
PT preventing, e.g. cardiomyopathy, atherosclerosis, hypertension, obesity,
PT prostate cancer, diabetes, hemophilia, AIDS, inflammatory bowel disease,
PT or infectious disease.

XX Claim 1; SEQ ID NO 46; 206pp; English.
PS
XX This invention describes novel human NOVX polypeptides and the
CC polynucleotides encoding them. The therapeutic is useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease selected from pathology associated with the polypeptide.
CC Diseases include cardiomyopathy, atherosclerosis, hypertension, pulmonary
CC stenosis, obesity, prostate cancer, diabetes, haemophilia, skin
CC disorders, graft versus host disease, AIDS, asthma, lupus, Crohn's
CC disease, inflammatory bowel disease, ulcerative colitis, multiple
CC sclerosis, infectious disease, anorexia, Alzheimer's disease, or
CC Parkinson's disease. They are also useful in detection assays, chromosome
CC mapping, or tissue typing. This sequence represents the human NOV4e
XX protein.

SQ Sequence 347 AA;

Query Match 100.0%; Score 631; DB 8; Length 347;
Best Local Similarity 100.0%; Pred.No.1e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDLRLNDDAKRYSTPRNYSVNIREEELKLANVVFPRCLLVQRCGNGCGGTVNRSCT 60
Db |||||||
235 VDLRLNDDAKRYSTPRNYSVNIREEELKLANVVFPRCLLVQRCGNGCGGTVNRSCT 294
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERCDCICSSRP 113
Db |||||||
295 CNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERCDCICSSRP 347

Search completed: November 10, 2005, 09:31:33
Job time : 56.2774 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:47 ; Search time 14.0373 Seconds
(without alignments)
600.925 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370

Perfect score: 631

Sequence: 1 VLDRLNDKRYSCPRNY.....DIQLDHERCDCICSSRPPR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/prodata/1/iaa/PCITUS COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	302	4	US-09-564-595D-54
2	631	100.0	316	4	US-09-564-595D-55
3	631	100.0	322	4	US-09-438-046-6
4	631	100.0	370	4	US-09-457-066-37
5	631	100.0	370	4	US-09-540-224-2
6	631	100.0	370	4	US-09-564-595D-2
7	631	100.0	370	4	US-09-706-968-37
8	631	100.0	370	4	US-09-808-972-2
9	631	100.0	370	4	US-09-823-033-5
10	631	100.0	370	4	US-09-438-046-8
11	631	100.0	370	4	US-10-139-583-37
12	631	100.0	370	4	US-10-039-847A-2
13	607	96.2	121	4	US-09-438-046-18
14	607	96.2	200	4	US-09-438-046-4
15	588	93.2	370	4	US-09-540-224-4
16	588	93.2	370	4	US-09-564-595D-53
17	588	93.2	370	4	US-09-808-972-4
18	588	93.2	370	4	US-10-039-847A-4
19	300	60.2	66	4	US-09-438-046-2
20	320	50.7	374	4	US-09-468-647A-118
21	318.5	50.5	132	4	US-09-468-647A-29
22	318.5	50.5	149	4	US-09-468-647A-124
23	318.5	50.5	303	4	US-09-564-595D-57
24	318.5	50.5	317	4	US-09-564-595D-56
25	318.5	50.5	323	4	US-09-468-647A-1
26	318.5	50.5	345	4	US-09-040-220D-2
27	318.5	50.5	345	4	US-09-457-066-2

28	318.5	50.5	345	4	US-09-265-686-2	Sequence 2, Appl
29	318.5	50.5	345	4	US-09-540-224-5	Sequence 5, Appl
30	318.5	50.5	345	4	US-09-564-595D-33	Sequence 33, Appl
31	318.5	50.5	345	4	US-09-706-968-2	Sequence 2, Appl
32	318.5	50.5	345	4	US-09-723-749-2	Sequence 2, Appl
33	318.5	50.5	345	4	US-09-823-033-2	Sequence 2, Appl
34	318.5	50.5	345	4	US-09-468-647A-2	Sequence 2, Appl
35	318.5	50.5	345	4	US-09-468-647A-101	Sequence 101, App
36	318.5	50.5	345	4	US-09-468-647A-103	Sequence 103, App
37	318.5	50.5	345	4	US-09-468-647A-110	Sequence 110, App
38	318.5	50.5	345	4	US-09-468-647A-130	Sequence 130, App
39	318.5	50.5	345	4	US-10-139-583-2	Sequence 2, Appl
40	318.5	50.5	354	4	US-09-468-647A-120	Sequence 120, App
41	318.5	50.5	355	4	US-09-468-647A-122	Sequence 122, App
42	311.5	49.4	345	4	US-09-457-066-43	Sequence 43, Appl
43	311.5	49.4	345	4	US-09-564-595D-35	Sequence 35, Appl
44	311.5	49.4	345	4	US-09-706-968-43	Sequence 43, Appl
45	311.5	49.4	345	4	US-09-823-033-4	Sequence 4, Appl
46	311.5	49.4	345	4	US-10-139-583-43	Sequence 43, Appl
47	308.5	48.9	113	4	US-09-468-647A-99	Sequence 99, Appl
48	292	46.3	227	4	US-09-468-647A-114	Sequence 114, App
49	292	46.3	227	4	US-09-468-647A-116	Sequence 116, App
50	118	18.7	24	4	US-09-540-224-9	Sequence 9, Appl
51	118	18.7	24	4	US-09-564-595D-41	Sequence 41, Appl
52	118	18.7	24	4	US-09-808-972-11	Sequence 11, Appl
53	102	16.2	109	3	US-09-469-186-1	Sequence 1, Appl
54	102	16.2	109	4	US-09-469-185-1	Sequence 1, Appl
55	102	16.2	109	4	US-10-100-037-1	Sequence 1, Appl
56	102	16.2	197	4	US-09-431-888-8	Sequence 8, Appl
57	102	16.2	325	3	US-08-915-795-3	Sequence 3, Appl
58	102	16.2	325	4	US-09-296-273-3	Sequence 3, Appl
59	102	16.2	354	3	US-08-915-795-5	Sequence 5, Appl
60	102	16.2	354	4	US-09-296-275-5	Sequence 5, Appl
61	102	16.2	354	4	US-09-375-248-6	Sequence 6, Appl
62	102	16.2	354	4	US-09-468-647A-109	Sequence 109, App
63	102	16.2	354	4	US-09-169-079-22	Sequence 22, Appl
64	102	16.2	354	4	US-09-214-982-1	Sequence 1, Appl
65	102	16.2	362	4	US-09-949-016-11286	Sequence 11286, A
66	100	15.8	110	4	US-09-847-524-6	Sequence 6, Appl
67	100	15.8	321	3	US-08-915-795-9	Sequence 9, Appl
68	100	15.8	321	4	US-09-847-524-4	Sequence 4, Appl
69	100	15.8	321	4	US-09-296-275-9	Sequence 9, Appl
70	100	15.8	358	3	US-08-915-795-8	Sequence 8, Appl
71	100	15.8	358	4	US-09-847-524-2	Sequence 2, Appl
72	100	15.8	358	4	US-09-296-275-8	Sequence 8, Appl
73	100	15.8	358	4	US-09-438-046-15	Sequence 15, Appl
74	95.5	15.1	102	1	US-08-469-427A-2	Sequence 2, Appl
75	95.5	15.1	102	2	US-08-609-443B-2	Sequence 2, Appl
76	95.5	15.1	102	2	US-08-569-063C-2	Sequence 2, Appl
77	95.5	15.1	102	3	US-08-851-896-2	Sequence 2, Appl
78	95.5	15.1	133	1	US-08-469-427A-9	Sequence 9, Appl
79	95.5	15.1	133	2	US-08-609-443B-9	Sequence 9, Appl
80	95.5	15.1	133	2	US-08-569-063C-9	Sequence 9, Appl
81	95.5	15.1	133	3	US-08-851-896-9	Sequence 9, Appl
82	95.5	15.1	188	1	US-08-469-427A-5	Sequence 5, Appl
83	95.5	15.1	188	2	US-08-609-443B-5	Sequence 5, Appl
84	95.5	15.1	188	3	US-08-569-063C-5	Sequence 5, Appl
85	95.5	15.1	188	3	US-08-851-896-5	Sequence 5, Appl
86	95.5	15.1	207	2	US-08-609-443B-13	Sequence 13, Appl
87	95.5	15.1	207	2	US-08-569-063C-13	Sequence 13, Appl
88	95.5	15.1	207	3	US-08-851-896-13	Sequence 13, Appl
89	94	14.9	195	1	US-08-469-427A-7	Sequence 7, Appl
90	94	14.9	195	2	US-08-609-443B-7	Sequence 7, Appl
91	94	14.9	195	3	US-08-569-063C-7	Sequence 7, Appl
92	94	14.9	195	3	US-08-851-896-7	Sequence 7, Appl
93	93	14.7	228	4	US-09-431-888-7	Sequence 7, Appl
94	93	14.7	350	2	US-08-999-811-4	Sequence 4, Appl
95	93	14.7	350	2	US-08-824-996-2	Sequence 2, Appl
96	93	14.7	350	3	US-09-042-105-4	Sequence 4, Appl
97	93	14.7	350	3	US-08-510-133A-33	Sequence 33, Appl
98	93	14.7	350	3	US-08-585-895-33	Sequence 33, Appl
99	93	14.7	350	4	US-10-084-488-4	Sequence 4, Appl
100	93	14.7	419	2	US-08-999-811-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-564-595D-54
; Sequence 54, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

Query Match 100.0%; Score 631; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.4e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGCGCTVNRSC 60
DB 190 VDLRLNDADKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGCGCTVNRSC 249
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 250 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 302

RESULT 2

US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match 100.0%; Score 631; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGCGCTVNRSC 60
DB 204 VDLRLNDADKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGCGCTVNRSC 263
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 264 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 316

RESULT 3

US-09-438-046-6
; Sequence 6, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-6

Query Match 100.0%; Score 631; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.8e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGCGCTVNRSC 60
DB 210 VDLRLNDADKRYSCYTPRNSVNIREEELKLANVFFPRCLLVQRCGCGCTVNRSC 269
QY 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 270 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 322

RESULT 4

US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.

```
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-37

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317
QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 5
US-09-540-224-2
; Sequence 2, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317
QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 6
US-09-564-595D-2
; Sequence 2, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa.
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D

; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-2

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317
QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 7
US-09-706-968-37
; Sequence 37, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-37

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 258 VDLRLNDKAKRYSCPTPRNYSVNIRELKLANVVFPRCLLVORCGNCGCGTVNWRSC 317
QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 318 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 8
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
```

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; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROBLASTIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2

Query Match          100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 60
DB 258 VDLRLNDKAKYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 317

QY 61 CNSGKTVKXHYEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTVKXHYEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 9
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5

Query Match          100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 60
DB 258 VDLRLNDKAKYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 317

QY 61 CNSGKTVKXHYEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTVKXHYEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 370

RESULT 10
US-09-438-046-8
; Sequence 8, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuzi
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44633
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-8

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Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 258 VDLRLNDKAKYCTPRNYSVNIREEKLANVFFPRCLLVQRCGNGCGGTVNRSC 317

QY 61 CNSGKTVKXHYEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 113
DB 318 CNSGKTVKXHYEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 370
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    |||||

QY 61 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 113
    |||||
Db 318 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 370
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RESULT 12
US-10-039-847A-2
; Sequence 2, Application US/1003987A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; .TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match      100.0%; Score 631; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 5.7e-66;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIIEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
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QY 61 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 113
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RESULT 13
US-09-438-046-18
; Sequence 18, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 200
; .TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-4

Query Match      96.2%; Score 607; DB 4; Length 200;
Best Local Similarity 97.3%; Pred. No. 1.8e-63;
Matches 110; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIIEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
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    |||||

QY 61 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 113
    |||||
Db 148 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 200
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Query Match      96.2%; Score 607; DB 4; Length 121;
Best Local Similarity 97.3%; Pred. No. 9.7e-64;
Matches 110; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIIEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
    |||||
Db 9 VDLRLNDADAKRYSCPTPNYSVNIIEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 68
    |||||

QY 61 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 113
    |||||
Db 69 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 121
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RESULT 14
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; Sequence 4, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 200
; .TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-4

Query Match      96.2%; Score 607; DB 4; Length 200;
Best Local Similarity 97.3%; Pred. No. 1.8e-63;
Matches 110; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDLRLNDADAKRYSCPTPNYSVNIIEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
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Db 88 VDLRLNDADAKRYSCPTPNYSVNIIEELKLANVVFPRCLLVORCGNCGCGTVNWRSC 147
    |||||

QY 61 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 113
    |||||
Db 148 CNSGKTVKKYHEVLQPEPGHKKRGRKTMALVDIQLDHHRCDCICSSRPPR 200
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RESULT 15
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4

Query Match          93.2%; Score 588; DB 4; Length 370;
Best Local Similarity 90.3%; Pred. No. 6,5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0

Qy 1 VDLRLNDDAKRYSGTSPNYSVNTREELKLVANVFFPRCLLVQRCGNCGGCTVNRSGT 60
Db 258 VDLRLNDVVKRYSGTSPNHSVNTREELKLTNAVFFPRCLLVQRCGNCGGCTVNRSGT 317

Qy 61 CNSGKTVKKYHEVLQFEPGHTKRGRKTMALVDIQLDHHERCDCICSSRP 113
Db 318 CSSGKTVKKYHEVLKFPFGHFKRGRKAKNMALVDIQLDHHERCDCICSSRP 370

RESULT 16
US-09-564-595D-53
; Sequence 53, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-595D-53

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RESULT 17
US-09-808-972-4
; Sequence 4, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Glibertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4

Query Match          93.2%; Score 588; DB 4; Length 370;
Best Local Similarity 90.3%; Pred. No. 6.5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy      1  VDRLRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVORCGNCGGTNNRSCT 60
Db      258 VDRLRLNDDVKRYSCTPRNHNSVNLREELKLTNAVFFPRCLLVORCGNCGGTNNKSCT 317

Qy      61  CNSGKTVKHYEVLQEPFGHFKERGRAKTMALVDIQLDHHERCDCICSSRPPR 113
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RESULT 18
US-10-039-847A-4
; Sequence 4, Application US/10039847A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-039-847A-4

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Query Match 93.2%; Score 588; DB 4; Length 370;
Best Local Similarity 90.3%; Pred. No. 6.5e-61;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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Db 258 VDLRLNDVVKYSCPRNHSVNLREELKLTNAVFPFRCLLVQRCGGNCGCGTVMWKSCT 317
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Db 318 CMSGKTVKXKYEVLQFEPGHFKRGRKAKMALVDIQLDHHRCDCICSSRRPR 370

RESULT 19

US-09-438-046-2
; Sequence 2, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annika
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438, 046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-2

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Best Local Similarity 100.0%; Pred. No. 2.3e-37;
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Qy 108 SSRPR 113
Db 61 SSRPR 66

RESULT 20

US-09-468-647A-118
; Sequence 118, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Von, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiowska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: GB 9828377.3

; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-118
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Best Local Similarity 51.3%; Pred. No. 2.2e-29;
Matches 60; Conservative 14; Mismatches 35; Indels 8; Gaps 2;
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Db 236 VDLRLNLTBEVRLYSCPRNHSVNLREELKLTNAVFPFRCLLVQRCGGNCGCGTVMWKSCT 295
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(without alignments)
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Perfect score: 631

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Maximum Match 100%

Listing first 100 summaries

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SUMMARIES

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2	631	100.0	132	14 US-10-011-364-6	Sequence 6, Appl
3	631	100.0	132	15 US-10-321-962-6	Sequence 6, Appl
4	631	100.0	132	16 US-10-403-142-38	Sequence 38, Appl
5	631	100.0	132	20 US-11-096-308-4	Sequence 4, Appl
6	631	100.0	152	15 US-10-276-774-2067	Sequence 2067, Ap
7	631	100.0	154	14 US-10-011-364-12	Sequence 12, Appl
8	631	100.0	154	15 US-10-321-962-12	Sequence 12, Appl
9	631	100.0	302	11 US-09-876-813-54	Sequence 54, Appl
10	631	100.0	302	16 US-10-877-623-54	Sequence 54, Appl
11	631	100.0	316	11 US-09-876-813-55	Sequence 55, Appl

12	631	100.0	316	16 US-10-877-623-55	Sequence 55, Appl
13	631	100.0	317	13 US-10-083-853-2	Sequence 2, Appl
14	631	100.0	322	13 US-10-086-623-6	Sequence 6, Appl
15	631	100.0	322	14 US-10-260-539-6	Sequence 6, Appl
16	631	100.0	322	18 US-10-794-392-6	Sequence 6, Appl
17	631	100.0	347	16 US-10-403-142-46	Sequence 46, Appl
18	631	100.0	364	14 US-10-028-072-186	Sequence 186, App
19	631	100.0	364	14 US-10-140-808-186	Sequence 186, App
20	631	100.0	364	14 US-10-121-049-186	Sequence 186, App
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31	631	100.0	364	14 US-10-123-262-186	Sequence 186, App
32	631	100.0	364	14 US-10-142-423-186	Sequence 186, App
33	631	100.0	364	14 US-10-121-050-186	Sequence 186, App
34	631	100.0	364	14 US-10-141-755-186	Sequence 186, App
35	631	100.0	364	14 US-10-143-032-186	Sequence 186, App
36	631	100.0	364	14 US-10-123-108-186	Sequence 186, App
37	631	100.0	364	14 US-10-123-236-186	Sequence 186, App
38	631	100.0	364	14 US-10-123-261-186	Sequence 186, App
39	631	100.0	364	14 US-10-140-921-186	Sequence 186, App
40	631	100.0	364	14 US-10-140-928-186	Sequence 186, App
41	631	100.0	364	14 US-10-121-045-186	Sequence 186, App
42	631	100.0	364	14 US-10-123-292-186	Sequence 186, App
43	631	100.0	364	14 US-10-123-903-186	Sequence 186, App
44	631	100.0	364	14 US-10-124-819-186	Sequence 186, App
45	631	100.0	364	14 US-10-124-822-186	Sequence 186, App
46	631	100.0	364	14 US-10-140-925-186	Sequence 186, App
47	631	100.0	364	14 US-10-160-498-186	Sequence 186, App
48	631	100.0	364	14 US-10-124-824-186	Sequence 186, App
49	631	100.0	364	14 US-10-127-825A-186	Sequence 186, App
50	631	100.0	364	14 US-10-127-829A-186	Sequence 186, App
51	631	100.0	364	14 US-10-127-835A-186	Sequence 186, App
52	631	100.0	364	14 US-10-127-839A-186	Sequence 186, App
53	631	100.0	364	14 US-10-127-901A-186	Sequence 186, App
54	631	100.0	364	14 US-10-128-693A-186	Sequence 186, App
55	631	100.0	364	14 US-10-131-813A-186	Sequence 186, App
56	631	100.0	364	14 US-10-131-818A-186	Sequence 186, App
57	631	100.0	364	14 US-10-131-823A-186	Sequence 186, App
58	631	100.0	364	14 US-10-131-824A-186	Sequence 186, App
59	631	100.0	364	14 US-10-131-830A-186	Sequence 186, App
60	631	100.0	364	14 US-10-137-872A-186	Sequence 186, App
61	631	100.0	364	14 US-10-147-500-186	Sequence 186, App
62	631	100.0	364	14 US-10-147-502-186	Sequence 186, App
63	631	100.0	364	14 US-10-147-515-186	Sequence 186, App
64	631	100.0	364	14 US-10-147-517-186	Sequence 186, App
65	631	100.0	364	14 US-10-147-526-186	Sequence 186, App
66	631	100.0	364	14 US-10-147-527-186	Sequence 186, App
67	631	100.0	364	14 US-10-121-041-186	Sequence 186, App
68	631	100.0	364	14 US-10-121-043-186	Sequence 186, App
69	631	100.0	364	14 US-10-121-047-186	Sequence 186, App
70	631	100.0	364	14 US-10-121-215-186	Sequence 186, App
71	631	100.0	364	14 US-10-123-902-186	Sequence 186, App
72	631	100.0	364	14 US-10-123-908-186	Sequence 186, App
73	631	100.0	364	14 US-10-123-909-186	Sequence 186, App
74	631	100.0	364	14 US-10-123-910-186	Sequence 186, App
75	631	100.0	364	14 US-10-124-813-186	Sequence 186, App
76	631	100.0	364	14 US-10-124-817-186	Sequence 186, App
77	631	100.0	364	14 US-10-125-922-186	Sequence 186, App
78	631	100.0	364	14 US-10-125-924-186	Sequence 186, App
79	631	100.0	364	14 US-10-140-860-186	Sequence 186, App
80	631	100.0	364	14 US-10-142-417-186	Sequence 186, App
81	631	100.0	364	14 US-10-147-519-186	Sequence 186, App
82	631	100.0	364	14 US-10-157-782-186	Sequence 186, App
83	631	100.0	364	14 US-10-152-395-186	Sequence 186, App

85 631 100.0 364 14 US-10-125-926A-186 Sequence 186, App
86 631 100.0 364 14 US-10-125-930A-186 Sequence 186, App
87 631 100.0 364 14 US-10-127-831A-186 Sequence 186, App
88 631 100.0 364 14 US-10-127-837A-186 Sequence 186, App
89 631 100.0 364 14 US-10-127-838B-186 Sequence 186, App
90 631 100.0 364 14 US-10-127-842A-186 Sequence 186, App
91 631 100.0 364 14 US-10-127-843A-186 Sequence 186, App
92 631 100.0 364 14 US-10-127-845A-186 Sequence 186, App
93 631 100.0 364 14 US-10-127-846A-186 Sequence 186, App
94 631 100.0 364 14 US-10-127-848A-186 Sequence 186, App
95 631 100.0 364 14 US-10-127-849A-186 Sequence 186, App
96 631 100.0 364 14 US-10-127-850A-186 Sequence 186, App
97 631 100.0 364 14 US-10-127-851A-186 Sequence 186, App
98 631 100.0 364 14 US-10-128-684A-186 Sequence 186, App
99 631 100.0 364 14 US-10-128-686A-186 Sequence 186, App
100 631 100.0 364 14 US-10-128-690A-186 Sequence 186, App

ALIGNMENTS

RESULT 1
US-10-403-142-42
; Sequence 42, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573A
; CURRENT APPLICATION NUMBER: US/10/403,142
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 08/969106
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/688598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/894159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 42
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-142-42

Query Match 100.0%; Score 631; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.8e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRGGNCGGTVNRSC 60
Db 11 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRGGNCGGTVNRSC 70
Oy 61 CNSGKTVKHYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 113
Db 71 CNSGKTVKHYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 123

RESULT 2
US-10-011-364-6
; Sequence 6, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry
; APPLICANT: Jeffers, Michael
; APPLICANT: Shimkets, Richard
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Boldog, Ferenc
; APPLICANT: Yang, Meijia
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Rittman, B.
; APPLICANT: Shimkets, Juliette
; APPLICANT: Larocheille, William
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth
; FILE REFERENCE: 15966-557A IBD CIP
; CURRENT APPLICATION NUMBER: US/10/011,364
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/246,206
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/992,840
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-364-6

Query Match 100.0%; Score 631; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRGGNCGGTVNRSC 60
Db 20 VDLRLNDKRYCTPRNYSVNIREELKLANVVFPRCLLVQRGGNCGGTVNRSC 79
Oy 61 CNSGKTVKHYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 113
Db 80 CNSGKTVKHYHEVLQFEFGHIKRRGRKTMALVDIQLDHHERCDCICSSRPP 132

RESULT 3
US-10-321-962-6
; Sequence 6, Application US/10321962
; Publication No. US20040006015A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Fernandes, Elma
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Larocheille, William J.
; APPLICANT: Lichenstein, Henry S.
; APPLICANT: Peterson, Jeffrey
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Rittman, Beth
; APPLICANT: Shimkets, Juliette
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Yang, Meijia
; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
; FILE REFERENCE: 15966-557A IBD CIP2
; CURRENT APPLICATION NUMBER: US/10/321,962
; CURRENT FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
; LENGTH: 132

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962-6

Query Match          100.0%; Score 631; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCCTPRNYSVNIIEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
   |||||||
Db 20 VDLRLNDKAKYSCCTPRNYSVNIIEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 79
   |||||||

QY 61 CMSGKTVKXYHEVLOPEGHKRRGRAKTMALVDIQLDHHRCDCICSSRRPPR 113
   |||||||
Db 80 CMSGKTVKXYHEVLOPEGHKRRGRAKTMALVDIQLDHHRCDCICSSRRPPR 132
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RESULT 4
US-10-403-142-38
; Sequence 38, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573A
; CURRENT APPLICATION NUMBER: US/10/403,142
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 08/969106
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/688598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/894159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 38
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-142-38

Query Match          100.0%; Score 631; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCCTPRNYSVNIIEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
   |||||||
Db 20 VDLRLNDKAKYSCCTPRNYSVNIIEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 79
   |||||||

QY 61 CMSGKTVKXYHEVLOPEGHKRRGRAKTMALVDIQLDHHRCDCICSSRRPPR 113
   |||||||
Db 80 CMSGKTVKXYHEVLOPEGHKRRGRAKTMALVDIQLDHHRCDCICSSRRPPR 132
   |||||||

RESULT 5
US-11-096-308-4
; Sequence 4, Application US/11096308
; Publication No. US20050171020A1
```

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; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Herrmann, John
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Growth Factor Polypeptides and Nucleic Acids Encoding
; TITLE OF INVENTION: Same
; FILE REFERENCE: 15966-577 CON (Cura-77 CON)
; CURRENT APPLICATION NUMBER: US/11/096,308
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: USSN 09/662,783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: USSN 60/158,083
; PRIOR FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: USSN 60/186,707
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: USSN 60/188,250
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: USSN 60/159,231
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: USSN 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: USSN 60/223,879
; PRIOR FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-308-4

Query Match          100.0%; Score 631; DB 20; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCCTPRNYSVNIIEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
   |||||||
Db 20 VDLRLNDKAKYSCCTPRNYSVNIIEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 79
   |||||||

QY 61 CMSGKTVKXYHEVLOPEGHKRRGRAKTMALVDIQLDHHRCDCICSSRRPPR 113
   |||||||
Db 80 CMSGKTVKXYHEVLOPEGHKRRGRAKTMALVDIQLDHHRCDCICSSRRPPR 132
   |||||||

RESULT 6
US-10-276-774-2067
; Sequence 2067, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2067
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2067

Query Match          100.0%; Score 631; DB 15; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.5e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKYSCCTPRNYSVNIIEELKLANVVFPRCLLVQRCGCGCGTNNRSCT 60
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Db 40 VDLRLNDADAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGGTVNRSC 99
Qy 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113
Db 100 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 152

RESULT 7

US-10-011-364-12
; Sequence 12, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry
; APPLICANT: Jeffers, Michael
; APPLICANT: Shinkets, Richard
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Boldog, Ferenc
; APPLICANT: Yang, Meijia
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Rittman, B.
; APPLICANT: Shinkets, Juliette
; APPLICANT: Larochele, William
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth

; TITLE OF INVENTION: Factors
; FILE REFERENCE: 15966-557A IBD CIP
; CURRENT APPLICATION NUMBER: US/10/011,364
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/246,206
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/992,840
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 12
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-364-12

Query Match 100.0%; Score 631; DB 14; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGGTVNRSC 60
Db 42 VDLRLNDADAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGGTVNRSC 101

Qy 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113

Db 102 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 154

RESULT 8

US-10-321-962-12
; Sequence 12, Application US/10321962
; Publication No. US20040006015A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Fernandes, Elma
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Larochele, William J.
; APPLICANT: Lichenstein, Henry S.
; APPLICANT: Peterson, Jeffrey
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Rittman, Beth
; APPLICANT: Shinkets, Juliette
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Yang, Meijia
; APPLICANT: CuraGen Corporation
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease

; TITLE OF INVENTION: Using Growth Factors
; FILE REFERENCE: 15966-557A IBD CIP2
; CURRENT APPLICATION NUMBER: US/10/321,962
; CURRENT FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962-12

Query Match 100.0%; Score 631; DB 15; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGGTVNRSC 60
Db 42 VDLRLNDADAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGGTVNRSC 101

Qy 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113

Db 102 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 154

RESULT 9

US-09-876-813-54
; Sequence 54, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-54

Query Match 100.0%; Score 631; DB 11; Length 302;
Best Local Similarity 100.0%; Pred. No. 7.5e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDLRLNDADAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGGTVNRSC 60
Db 190 VDLRLNDADAKRYCTPRNYSVNIREELKLANVFFPRCLLVQRCGGCGGTVNRSC 249

Qy 61 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 113

Db 250 CNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERCDCICSSRPPR 302

RESULT 10

US-10-877-623-54
; Sequence 54, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:

```

; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
;
US-10-877-623-54

Query Match          100.0%; Score 631; DB 16; Length 302;
Best Local Similarity 100.0%; Pred. No. 7.5e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLDRLNDKAKYSCCTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWSCT 60
Db 190 VLDRLNDKAKYSCCTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWSCT 249

QY 61 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 250 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 302

RESULT 11
US-09-876-813-55
; Sequence 55, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
;
US-09-876-813-55

Query Match          100.0%; Score 631; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLDRLNDKAKYSCCTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWSCT 60
Db 190 VLDRLNDKAKYSCCTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWSCT 249

QY 61 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 250 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 302

RESULT 12
US-10-877-623-55
; Sequence 55, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
;
US-10-877-623-55

Query Match          100.0%; Score 631; DB 16; Length 316;
Best Local Similarity 100.0%; Pred. No. 7.9e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLDRLNDKAKYSCCTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWSCT 60
Db 204 VLDRLNDKAKYSCCTPRNYSVNIREEELKLANVVFPRCLLVORCGNCGCGTVNWSCT 263

QY 61 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 113
Db 264 CNSGKTVKKYHEVLOPEPGHKKRRGAKTMALVDIQLDHHERCDCICSSRPPR 316

RESULT 13
US-10-083-853-2
; Sequence 2, Application US/10083853
; Publication No. US20020164709A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc
; APPLICANT: Shigeta, Ron T
; APPLICANT: Siani-Rose, Michael A
; TITLE OF INVENTION: Nucleic Acid Encoding Growth Factor Protein
; FILE REFERENCE: 3385.1
; CURRENT APPLICATION NUMBER: US/10/083,853
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: USSN 60/272,663
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 317
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; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-392-6

Query Match      100.0%; Score 631; DB 18; Length 322;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLDRLNDADKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 210 VLDRLNDADKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 269

QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIOLDHHERCDICSSRPPR 113
Db 270 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIOLDHHERCDICSSRPPR 322

RESULT 17
US-10-403-142-46
; Sequence 46, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Aleobrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573A
; CURRENT APPLICATION NUMBER: US/10/403,142
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 08/969106
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/688598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/894159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 46
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-142-46

Query Match      100.0%; Score 631; DB 16; Length 347;
Best Local Similarity 100.0%; Pred. No. 8.7e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLDRLNDADKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
Db 235 VLDRLNDADKRYSCPTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 294

QY 61 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIOLDHHERCDICSSRPPR 113
Db 295 CMSGKTVKKYHEVLQEPGHIKRRGAKTMALVDIOLDHHERCDICSSRPPR 347

RESULT 18
US-10-028-072-186
; Sequence 186, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR FILING DATE: 1997-09-19
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; PRIOR FILING DATE: 1997-09-19
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; PRIOR FILING DATE: 1997-09-24
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; PRIOR FILING DATE: 1997-10-29
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; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
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; PRIOR FILING DATE: 1998-02-09
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; PRIOR APPLICATION NUMBER: 60/080165
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; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 631; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSTPRNYSNIREELKLANVFFPRCLLVORCGGCGCTVNRST 60
DB 252 VDLRLNDKAKRYSTPRNYSNIREELKLANVFFPRCLLVORCGGCGCTVNRST 311
QY 61 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 312 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 364

RESULT 19

US-10-140-808-186
; Sequence 186, Application US/10140808
; Publication No. US20030017563A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 186
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-186

Query Match 100.0%; Score 631; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSTPRNYSNIREELKLANVFFPRCLLVORCGGCGCTVNRST 60
DB 252 VDLRLNDKAKRYSTPRNYSNIREELKLANVFFPRCLLVORCGGCGCTVNRST 311
QY 61 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 312 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 364

RESULT 20

US-10-121-049-186
; Sequence 186, Application US/10121049
; Publication No. US2003002239A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 186
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-186

Query Match 100.0%; Score 631; DB 14; Length 364;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDLRLNDKAKRYSTPRNYSNIREELKLANVFFPRCLLVORCGGCGCTVNRST 60
DB 252 VDLRLNDKAKRYSTPRNYSNIREELKLANVFFPRCLLVORCGGCGCTVNRST 311
QY 61 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
DB 312 CNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHHRCDCICSSRPPR 364

Search completed: November 10, 2005, 09:41:03
Job time : 52.7039 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:01 ; Search time 11.9317 Seconds
(without alignments)
911.229 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370

Perfect score: 631

Sequence: 1 VLDRLNDKAKRYSCPRNY.....DIQLDHERCDCICSSRPPR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	370	2	JC7591 spinal cord-derive
2	588	93.2	370	2	JC7998 platelet-derived g
3	585	92.7	370	2	JC7592 spinal cord-derive
4	100.5	15.9	148	2	D49530 16K vascular endot
5	95.5	15.1	188	2	JC4680 vascular endotheli
6	95.5	15.1	207	2	JC4679 vascular endotheli
7	94	14.9	166	2	JN0248 platelet-derived g
8	94	14.9	198	2	JS0735 platelet-derived g
9	93	14.7	419	2	S69207 vascular endotheli
10	89	14.1	196	2	A37359 platelet-derived g
11	89	14.1	196	2	A48851 platelet-derived g
12	89	14.1	196	2	B28964 platelet-derived g
13	89	14.1	197	2	S25096 platelet-derived g
14	89	14.1	211	1	PFHUG1 platelet-derived g
15	84.5	13.4	133	2	B49530 vascular endotheli
16	83.5	13.2	80	2	T03404 metallothionein-li
17	83	13.2	200	2	IS1551 platelet-derived g
18	83	13.2	215	2	S08220 platelet-derived g
19	83	13.2	226	2	IS1550 platelet-derived g
20	79	12.5	241	1	PFMSG8 platelet-derived g
21	78.5	12.4	80	2	T02063 metallothionein-li
22	78	12.4	225	2	S25097 platelet-derived g
23	78	12.4	297	2	G71265 hypothetical prote
24	77	12.2	77	2	S52636 metallothionein -
25	77	12.2	120	2	A33787 ovine vascular end
26	77	12.2	146	2	S57956 vascular endotheli
27	77	12.2	190	2	B40080 vascular endotheli
28	77	12.2	245	1	TVCITSS platelet-derived g
29	76	12.0	241	1	PFHUG2 platelet-derived g

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metallothionein -
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gonadotropin beta
gonadotropin II be
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hypothetical prote
DnI7 protein - yea
60 kDa outer membr
Mutator-like trans
Probable ATPase (E
metallothionein 20

30 75 11.9 82 2 T07114
31 74 11.7 77 2 T12187
32 74 11.7 79 2 JQ2128
33 74 11.7 82 2 T07076
34 73.5 11.6 82 2 T03727
35 73.5 11.6 158 2 A56125
36 73 11.6 78 2 S48038
37 73 11.6 79 2 T17014
38 72.5 11.5 80 2 T12326
39 72 11.4 80 2 T10087
40 71.5 11.3 333 2 B45558
41 71.5 11.3 342 2 C45558
42 71.5 11.3 366 2 D45558
43 71.5 11.3 538 2 E96492
44 71.5 11.3 1717 1 A45558
45 71 11.3 77 2 S37239
46 71 11.3 190 2 A35987
47 71 11.3 190 2 S52130
48 70.5 11.2 175 2 S09098
49 70.5 11.2 149 2 A41236
50 70.5 11.2 561 2 T27318
51 70.5 11.2 626 2 T27319
52 70 11.1 80 2 T14387
53 70 11.1 81 1 SMUL
54 70 11.1 81 2 S57861
55 70 11.1 190 2 B44881
56 70 11.1 214 2 A44881
57 70 11.1 226 1 TVNVSS
58 69.5 11.0 894 2 T26149
59 69.5 11.0 910 2 A48403
60 69.5 11.0 920 2 T26147
61 69 10.9 84 2 T03787
62 69 10.9 232 2 A41551
63 68.5 10.9 75 2 T12188
64 68.5 10.9 396 2 T49109
65 68 10.8 72 2 T07073
66 68 10.8 73 2 T07109
67 68 10.8 74 2 T16979
68 68 10.8 309 1 A69073
69 68 10.8 389 2 G75042
70 68 10.8 478 2 H71345
71 67.5 10.7 858 1 JQ1677
72 67 10.6 71 2 S47577
73 66.5 10.5 117 2 F97174
74 66.5 10.5 128 2 IS1295
75 66 10.5 71 2 S39422
76 66 10.5 77 2 S57862
77 66 10.5 84 2 T07115
78 65.5 10.4 400 2 T46383
79 65.5 10.4 723 2 PN0509
80 65.5 10.4 773 2 D86268
81 65.5 10.4 2907 2 A57278
82 65 10.3 72 2 T07105
83 65 10.3 142 2 IS0143
84 65 10.3 271 2 A25669
85 65 10.3 352 2 T47820
86 65 10.3 721 2 H82528
87 64.5 10.2 473 2 T45954
88 64.5 10.2 1790 1 MPFFB1
89 64.5 10.2 3020 2 A43932
90 64 10.1 60 2 T09258
91 64 10.1 113 1 S07092
92 64 10.1 140 2 A48166
93 64 10.1 152 2 T18975
94 64 10.1 680 2 PN0510
95 63.5 10.1 349 2 T20202
96 63.5 10.1 430 2 S61118
97 63.5 10.1 554 2 C81671
98 63.5 10.1 849 2 H84668
99 63.5 10.1 1612 2 S51243
100 63 10.0 71 2 S39421

See Derived !!

C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4680
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjoeld, M.; Weber, G.; Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A:Title: Characterization of the murine VEGF-related factor gene.
A:Reference number: JC4679; MUID:96183052; PMID:8607868
A:Accession: JC4680
A:Molecule type: mRNA
A:Cross-references: UNIPROT:P49766; GB:U43837; NID:G1314335; PIDN:AA052553.1; PID:G13143
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the VEGF family.
C:Genetics:
A:Gene: vrf
A:Map position: 19
A:Introns: 137/2
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-188/Product: vascular endothelial growth factor-related factor #status predicted <M>

Query Match 15.1%; Score 95.5; DB 2; Length 188;
Best Local Similarity 27.9%; Pred. No. 0.017;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 12 RYSCTPRNYSNIRELKLNVV--FFPRCLLVQRCGCGCTVNWRSCTNSGKTVKK 69
Db 44 RATCQPREVVPLSMEL-MGNVVKQLVPSCTVQRCG---GCCPDDGLECVPTGQHVQRM 99
QY 70 YHEVLQFEPGHKRRGRATKMTALVDIQLDHERCDCICSSRPP 113
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 6
JC4679
vascular endothelial growth factor-related factor 186 precursor - mouse
N:Alternate names: VRF 186 protein, VEGF 186
C:Species: Mus musculus (house mouse)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4679
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.; Nordenskjoeld, M.; Weber, G.; Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A:Title: Characterization of the murine VEGF-related factor gene.
A:Reference number: JC4679; MUID:96183052; PMID:8607868
A:Accession: JC4679
A:Molecule type: mRNA
A:Residues: 1-207 <TOW>
A:Cross-references: UNIPROT:P49766; GB:U43836; NID:G1703480; PIDN:AA052932.1; PID:G13143
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs to the VEGF family.
C:Genetics:
A:Gene: vrf
A:Map position: 19
C:Keywords: growth factor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-207/Product: vascular endothelial growth factor related factor #status predicted <M>

Query Match 15.1%; Score 95.5; DB 2; Length 207;
Best Local Similarity 27.9%; Pred. No. 0.018;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 12 RYSCTPRNYSNIRELKLNVV--FFPRCLLVQRCGCGCTVNWRSCTNSGKTVKK 69
Db 44 RATCQPREVVPLSMEL-MGNVVKQLVPSCTVQRCG---GCCPDDGLECVPTGQHVQRM 99
QY 70 YHEVLQFEPGHKRRGRATKMTALVDIQLDHERCDCICSSRPP 113
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 7
JN0248
platelet-derived growth factor chain A3 precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 27-Jun-1994
C:Accession: JN0248
R:Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascular endothelial cells.
A:Reference number: JN0248; MUID:92246970; PMID:1575749
A:Accession: JN0248
A:Molecule type: mRNA
A:Residues: 1-166 <NAK>
C:Superfamily: platelet-derived growth factor
F:1-22/Domain: propeptide (fragment) #status predicted <PRO>
F:23-166/Product: platelet-derived growth factor A3 chain #status predicted <MAT>

Query Match 14.9%; Score 94; DB 2; Length 166;
Best Local Similarity 28.0%; Pred. No. 0.021;
Matches 23; Conservative 17; Mismatches 32; Indels 10; Gaps 3;

QY 31 ANNVFFPRCLLVQRCGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHKRRGRATKM 90
Db 50 ANFLIWPPECVEVKRTGCC-----NTSSVKCQPSRVHHRSVKVAKE--YVRKKPKLKE- 101
QY 91 ALVDIQLDHERCDCICSSRPP 112
Db 102 --VQVRLBEHLECACAASSAGP 121

RESULT 8
JS0735
platelet-derived growth factor chain A1 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C:Accession: JS0735
R:Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascular endothelial cells.
A:Reference number: JN0248; MUID:92246970; PMID:1575749
A:Accession: JS0735
A:Molecule type: mRNA
A:Residues: 1-198 <NAK>
A:Cross-references: UNIPROT:P34007
A:Note: this protein corresponds to the endothelial type of human A chain
C:Superfamily: platelet-derived growth factor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-89/Domain: propeptide #status predicted <PRO>
F:90-198/Product: platelet-derived growth factor A1 chain #status predicted <MAT>

Query Match 14.9%; Score 94; DB 2; Length 198;
Best Local Similarity 28.0%; Pred. No. 0.025;
Matches 23; Conservative 17; Mismatches 32; Indels 10; Gaps 3;

QY 31 ANNVFFPRCLLVQRCGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHKRRGRATKM 90
Db 117 ANFLIWPPECVEVKRTGCC-----NTSSVKCQPSRVHHRSVKVAKE--YVRKKPKLKE- 168
QY 91 ALVDIQLDHERCDCICSSRPP 112
Db 169 --VQVRLBEHLECACAASSAGP 188

RESULT 9
S69207
vascular endothelial growth factor C precursor - human
N:Alternate names: FLT4 ligand DHM
C:Species: Homo sapiens (man)
C>Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S69207; S61795; S71443; S69208; G02859
R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chillov, D.; Lahinen, I.; Kukk, E.; Saksela, E.; EMBO J. 15, 1751, 1996
A:Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for VEGFR-2.
A:Reference number: S69207; MUID:96203094; PMID:8612600
A:Accession: S69207
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A;Residues: 1-419 <JOU>
A;Cross-references: UNIPROT:P49767; EMBL:X94216; NID:gl177488; PIDN:CAA63907.1; PID:e221
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, EMO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (V
A;Reference number: S61795; MUID:96178224; PMID:8617204
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 70-419 <JOU>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X', 104-120 <JOU>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and sp
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LES>
A;Cross-references: EMBL:U43142; NID:gl150988; PIDN:AAA85214.1; PID:gl150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U58111; NID:gl373426; PIDN:AAB02909.1; PID:gl373427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 14.7%; Score 93; DB 2; Length 419;
Best Local Similarity 20.7%; Pred. No. 0.062;
Matches 38; Conservative 20; Mismatches 50; Indels 76; Gaps 8;
Qy 3 LDRLNDKAKRYSCPRNYSVNIRELKLANVVF-PRCLLVQRCGNGC----- 50
Db 119 LKSIDNEWKTCQMPREVCIDVGKEFGVATNTFFKPCVYVYRCGCGCNSGLQCMNTST 178
Qy 51 -----CGTVNWSCTCNSGKTV-KKYHEVLQ----- 75
Db 179 SYLSKTLFEITVPLSQGPKPVTISFANHITSCRCNSKLDVYRQVHSIIRSLPATLPQCOA 238
Qy 76 -----FPGHITK-----RGRAKTMALVDI-----QLDHHERCDCICSS 109
Db 239 ANKTCPTNMYNNHICRCLAQDFMSSDAGDSDTDFGDFHICGPNKELD-BETQCVCRA 297
Qy 110 --RP 111
Db 298 GLRP 301

RESULT 10
A37359
platelet-derived growth factor chain A precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 07-May-1999
C;Accession: A37359
R;Mercola, M.; Wang, C.; Kelly, J.; Brownlee, C.; Jackson-Grusby, L.; Stiles, C.; Bowen-
Dev. Biol. 138, 114-122, 1990
A;Title: Selective expression of PDGF A and its receptor during early mouse embryogenesis
A;Reference number: A37359; MUID:90169294; PMID:2155144
A;Accession: A37359
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA
A;Residues: 1-196 <MER>
A;Cross-references: GB:M29464
C;Superfamily: platelet-derived growth factor

Query Match 14.1%; Score 89; DB 2; Length 196;
Best Local Similarity 26.8%; Pred. No. 0.081;
Matches 22; Conservative 18; Mismatches 32; Indels 10; Gaps 3;
Qy 31 ANVVFFPRCLLVQRCGNGCGGTVNRSCCTCNSGKTVKKYHEVLQFEPGHITKRRGRAKTM 90
Db 115 ANFLWPPCPVEVKRCTGCC-----NTSSVKQPSRVHRSYKVAKE--YVRKKPKLKE- 166
Qy 91 ALVDIQLDHHERCDCICSSRPP 112
Db 167 --VQVRLEEHLECACATSNLNP 186

RESULT 11
A48851
platelet-derived growth factor chain A precursor (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A48851; I51891
R;Katsuyose, D.; Ohe, M.; Yamauchi, K.; Ogata, M.; Shirato, K.; Fujita, H.; Shibahara, S.
Am. J. Physiol. 284, L100-L106, 1993
A;Title: Increased expression of PDGF A- and B-chain genes in rat lungs with hypoxic pul
A;Reference number: A48851; MUID:93191115; PMID:8447423
A;Accession: A48851
A;Molecule type: mRNA
A;Residues: 1-196 <KAT>
A;Cross-references: GB:D10106; NID:g220839; PIDN:BAA00987.1; PID:g220840
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:126515)
C;Superfamily: platelet-derived growth factor

Query Match 14.1%; Score 89; DB 2; Length 196;
Best Local Similarity 26.8%; Pred. No. 0.081;
Matches 22; Conservative 18; Mismatches 32; Indels 10; Gaps 3;
Qy 31 ANVVFFPRCLLVQRCGNGCGGTVNRSCCTCNSGKTVKKYHEVLQFEPGHITKRRGRAKTM 90
Db 115 ANFLWPPCPVEVKRCTGCC-----NTSSVKQPSRVHRSYKVAKE--YVRKKPKLKE- 166
Qy 91 ALVDIQLDHHERCDCICSSRPP 112
Db 167 --VQVRLEEHLECACATSNLNP 186

RESULT 12
B28964
platelet-derived growth factor chain A precursor splice form 2 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: B28964; B42002; B28122
R;Bonthon, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, a
A;Reference number: A28964; MUID:88144463; PMID:3422746
A;Accession: B28964
A;Molecule type: DNA
A;Residues: 1-196 <BON>
A;Cross-references: UNIPROT:P04085; GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M1998
R;Bonthon, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Spoleman, F.
Genomics 13, 257-263, 1992
A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA t
A;Reference number: A42002; MUID:92307656; PMID:1612586
A;Accession: B42002
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 152-196 <BO2>
R;Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988

R:Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A:Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, .
A:Reference number: A28964; MUID:88144463; PMID:3422746
A:Accession: A28964
A:Molecule type: DNA
A:Residues: 1-211 <BON>
A:Cross-references: UNIPROT:P04085; GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M1999
R:Takimoto, Y.; Kuramoto, A.
Biochim. Biophys. Acta 1222, 511-514, 1994
A:Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth fa
A:Reference number: S47564; MUID:94312450; PMID:7518695
A:Accession: S47564
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-21 <TAK>
R:Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A:Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA
A:Reference number: A42002; MUID:92307656; PMID:1612586
A:Accession: A42002
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 152-211 <BO2>
R:Beshtoltz, C.; Johnson, A.; Heldin, C.H.; Westermark, B.; Lind, P.; Urdea, M.S.; Eddy,
Nature 320, 695-699, 1986
A:Title: cDNA sequence and chromosomal localization of human platelet-derived growth fa
A:Reference number: A01379; MUID:86203630; PMID:3754619
A:Accession: A01379
A:Molecule type: mRNA
A:Residues: 1-211 <BET>
A:Cross-references: GB:X03795; NID:G35365; PIDN:CAA27421.1; PID:G35366
A:Experimental source: clonal glioma cell line U-343 MGaC12:6, a tumor cell line
R:Hoppe, J.; Schumacher, L.; Eichner, W.; Weich, H.A.
FEBS lett. 223, 243-246, 1987
A:Title: The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distantly
A:Reference number: S00173; MUID:88030061; PMID:3666150
A:Accession: S00173
A:Molecule type: mRNA
A:Residues: 1-193 'DVR' <HOP>
A:Cross-references: EMBL:X06374; NID:G35363; PIDN:CAA29677.1; PID:G35364
R:Korsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988
A:Title: Structural characterization of the human platelet-derived growth factor A-chain.
A:Reference number: A28122; MUID:88174698; PMID:2832727
A:Accession: A28122
A:Molecule type: mRNA
A:Residues: 1-63, 'TRD', 67-211 <ROR>
A:Cross-references: GB:M20488
A:Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65
C:Comment: platelet-derived growth factor, a potent mitogen for cells of mesenchymal or
C:Comment: A carboxyl-terminal propeptide may be removed from the precursor by proteoly
C:Genetics:
A:Gene: GDB:PDGFA
A:Cross-references: GDB:I20266; OMIM:173430
A:Map position: 7p22-7p22
A:Introns: 21/3; 54/1; 89/1; 151/3; 194/1
C:Complex: homodimer; heterodimer (see PIR:PFHUG2)
C:Superfamily: platelet-derived growth factor
C:Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-86/Domain: propeptide #status predicted <PRO>
F:87-211/Product: platelet-derived growth factor chain A #status predicted <MAT>
F:158-162/Region: receptor binding #status predicted
F:96-140,129-177,133-179/Disulfide bonds: #status predicted
F:123/Disulfide bonds: interchain (to chain B-133 in heterodimeric form) #status predic
F:132/Disulfide bonds: interchain (to chain B-124 in homodimeric form) #status predicted
F:132/Disulfide bonds: interchain (to chain B-124 in heterodimeric form) #status predic
F:133/Disulfide bonds: interchain (to 123 in homodimeric form) #status predicted
F:134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 89; DB 1; Length 211;
Best Local Similarity 26.8%; Pred. No. 0.087;

A:Reference number: I51550; MUID:88321676; PMID:3413486
A:Accession: I51550
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-226 <MER>
A:Cross-references: UNIPROT:P13698; GB:M23237; NID:G214648; PIDN:AAA49927.1; PID:G214649
C:Superfamily: platelet-derived growth factor

Query Match 13.2%; Score 83; DB 2; Length 226;
Best Local Similarity 26.6%; Pred. No. 0.38;
Matches 21; Conservative 18; Mismatches 30; Indels 10; Gaps 3;

QY 31 ANVFFPRCLLVORCGGCGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTM 90
DB 120 ANFLVPPCPEVKRGTGCC-----NTSSVKQCPRIHRSVRKAVE--YVRKPKLKE- 171

QY 91 ALVDIQLDHHERCDCICSS 109

DB 172 --VLVRLEEHLECTTANS 188

RESULT 20

PFMSG

platelet-derived growth factor chain B precursor (sis) - mouse
N:Alternate names: PDGF-related transforming protein
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1992 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A39073

R:Ronthron, D.T.; Sultan, P.; Collins, T.

Genomics 10, 287-292, 1991

A:Title: Structure of the murine c-sis proto-oncogene (Sis, PDGFB) encoding the B chain

A:Reference number: A39073; MUID:91257844; PMID:2045107

A:Accession: A39073

A:Molecule type: DNA

A:Residues: 1-241 <BON>

A:Cross-references: UNIPROT:P31240; GB:M64849; GB:M55394; NID:G192818; PIDN:AAA37485.1;

C:Genetics:

A:Gene: sis

C:Superfamily: platelet-derived growth factor

C:Keywords: glycoprotein; growth factor; platelet; proto-oncogene; transforming protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-81/Domain: propeptide #status predicted <PRO>

F:82-190/Product: platelet-derived growth factor chain B #status predicted <MAT>

F:159-163/Region: receptor binding #status predicted

F:63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.5%; Score 79; DB 1; Length 241;

Best Local Similarity 30.1%; Pred. No. 1;

Matches 25; Conservative 12; Mismatches 34; Indels 12; Gaps 3;

QY 31 ANVFFPRCLLVORCGGCGCTVNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTM 90
DB 116 ANFLVPPCPEVKRGTGCC-----NNRNVCASQVQVRKIEIVRKPIFKKATV 170

QY 91 ALVDIQLDHHERCDC--ICSSRP 111

DB 171 TLIED-----HLACKCETIVTPRP 188

Search completed: November 10, 2005, 09:36:11

Job time : 12.9317 secs

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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:21:06 ; Search time 51.0021 Seconds
(without alignments)
1134.561 Million cell updates/sec

Title: US-10-606-055-2_COPY_258_370

Perfect score: 631

Sequence: 1 VDLDRUNDARKYSTPRNY.....DIQLDHERCDCICSRPRP 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	364	Q9BWS5	Q9BWS5 homo sapien
2	631	100.0	370	Q9GZP0	Q9GZP0 homo sapien
3	588	92.7	370	Q9A5I7	Q9A5I7 mus musculus
4	585	92.7	370	Q9EOT1	Q9EOT1 rattus norv
5	511	81.0	300	Q6V9H4	Q6V9H4 oryctolagus
6	318.5	50.5	345	Q9NRA1	Q9NRA1 homo sapien
7	318.5	50.5	345	Q9UL22	Q9UL22 homo sapien
8	315.5	50.0	345	Q9I946	Q9I946 gallus gall
9	312.5	49.5	345	Q9EQX6	Q9EQX6 rattus norv
10	311.5	49.4	345	Q9QV71	Q9QV71 m fallotein
11	311.5	49.4	345	Q8CI19	Q8CI19 mus musculus
12	305.5	48.4	345	Q9JHV8	Q9JHV8 mus musculus
13	202	32.0	258	Q8K429	Q8K429 rattus norv
14	106.5	16.9	176	Q7QFM8	Q7QFM8 anophelies g
15	104	16.5	326	1 VEGD RAT	Q35251 rattus norv
16	104	16.5	326	Q912E4	Q912E4 rattus norv
17	102	16.2	194	Q6DC06	Q6DC06 brachydanio
18	102	16.2	354	1 VEGD_HUMAN	Q43915 homo sapien
19	100.5	15.9	148	1 VEGH_ORFN7	P52585 orf virus (
20	100	15.8	358	1 VEGD_MOUSE	P97946 mus musculus
21	99	15.7	149	Q6TVI8	Q6TVI8 orf virus.
22	97.5	15.5	252	2 Q8QGD7	Q8QGD7 gallus gall
23	95.5	15.1	135	1 VEGB RAT	Q35485 rattus norv
24	95.5	15.1	186	2 Q6DGF3	Q6DGF3 rattus norv
25	95.5	15.1	207	1 VEGB_MOUSE	P49766 mus musculus
26	95	15.1	146	1 TXVE BOTER	Q6J936 bothrops er
27	95	15.1	304	2 Q9N4I3	Q9N4I3 caenorhabdi
28	94	14.9	152	2 Q8B571	Q8B571 pseudocowpo
29	94	14.9	213	1 PDGA_RABIT	P34007 oryctolagus
30	93	14.7	146	1 TXVE_BOTIN	Q90X24 bothrops in
31	93	14.7	251	2 Q90W23	Q90W23 gallus gall

32	93	14.7	419	1	VEGC_HUMAN	P49767 homo sapien
33	93	14.7	419	2	Q6FH59	Q6FH59 homo sapien
34	92.5	14.7	396	2	Q7T3I6	Q7T3I6 brachydanio
35	92	14.6	146	1	TXVE BOTJA	Q90X23 bothrops la
36	92	14.6	405	2	Q9VM43	Q9VM43 drosophila
37	92	14.6	415	1	VEGC_MOUSE	P97953 mus musculus
38	92	14.6	415	2	Q91ZE3	Q91ZE3 rattus norv
39	91.5	14.5	326	2	Q91ZH6	Q91ZH6 meriones un
40	89	14.1	118	2	Q9CU96	Q9CU96 mus musculus
41	89	14.1	196	2	Q99L56	Q99L56 mus musculus
42	89	14.1	204	1	PDGA_RAT	P28576 rattus norv
43	89	14.1	211	1	PDGA_HUMAN	P04085 homo sapien
44	89	14.1	211	1	PDGA_MOUSE	P20033 mus musculus
45	89	14.1	211	2	Q6P7C3	Q6P7C3 rattus norv
46	89	14.1	211	2	Q7TPH7	Q7TPH7 mus musculus
47	89	14.1	418	2	O57352	O57352 coturnix co
48	88.5	14.0	314	2	O57352	O57352 coturnix co
49	88.5	14.0	325	2	Q9VMP6	Q9VMP6 drosophila
50	88	13.9	149	2	Q9WVQ7	Q9WVQ7 mesocricetu
51	87	13.8	420	2	Q9XS50	Q9XS50 bos taurus
52	86.5	13.7	195	2	Q9DE50	Q9DE50 brachydanio
53	86.5	13.7	207	1	VEGB_BOVIN	Q9X549 bos taurus
54	85.5	13.5	79	2	Q9FQ79	Q9FQ79 musa acumin
55	85.5	13.5	132	2	Q772M8	Q772M8 orf virus s
56	85.5	13.5	132	2	Q9YMF3	Q9YMF3 orf virus.
57	85	13.5	148	2	O42571	O42571 xenopus lae
58	85	13.5	194	2	O42571	O42571 xenopus lae
59	84.5	13.4	79	2	O6PML4	O6PML4 populus bal
60	84.5	13.4	133	1	VEGH_ORFN2	P52584 orf virus (
61	84.5	13.4	146	1	TXVE_TRIFL	P67862 trimeresauru
62	84	13.3	137	2	Q6TVW8	Q6TVW8 orf virus.
63	83.5	13.2	80	2	O04107	O04107 oryza sativ
64	83.5	13.2	188	2	Q8TEV2	Q8TEV2 homo sapien
65	83.5	13.2	207	1	VEGB_HUMAN	P49765 homo sapien
66	83.5	13.2	213	2	Q6DDJ9	Q6DDJ9 xenopus lae
67	83	13.2	226	1	PDGA_XENLA	P13598 xenopus lae
68	83	13.2	346	2	Q674V2	Q674V2 podocoryne
69	82	13.0	191	1	VEGA_BITGA	P83906 bitis gabon
70	81.5	12.9	79	2	Q944W1	Q944W1 typha latif
71	81	12.8	77	2	Q75NH6	Q75NH6 pisum sativ
72	81	12.8	241	1	PDGB_SHEEP	Q95229 ovis aries
73	80.5	12.8	79	2	Q9AU16	Q9AU16 typha latif
74	80.5	12.8	344	2	Q9VY49	Q9VY49 drosophila
75	80	12.7	124	2	Q8XIQ7	Q8XIQ7 clostridium
76	80	12.7	164	1	VEGA_CAVPO	P26617 cavia porce
77	80	12.7	194	2	Q90WK1	Q90WK1 gallus gall
78	80	12.7	198	2	Q90WK3	Q90WK3 gallus gall
79	80	12.7	211	2	Q90WK2	Q90WK2 gallus gall
80	79	12.5	219	2	Q8R3X9	Q8R3X9 mus musculus
81	79	12.5	241	1	PDGB_MOUSE	P31240 mus musculus
82	78.5	12.4	79	2	Q75NH9	Q75NH9 phaseolus a
83	78.5	12.4	79	2	Q75NI3	Q75NI3 phaseolus a
84	78.5	12.4	80	2	O22488	O22488 oryza sativ
85	78.5	12.4	110	1	TXVE_VIPLE	P82475 vipera lebe
86	78	12.4	108	2	Q8HY75	Q8HY75 ovis aries
87	78	12.4	211	2	Q9EUF7	Q9EUF7 gallus gall
88	78	12.4	225	1	PDGB_RAT	Q05028 rattus norv
89	78	12.4	241	2	Q6P3C4	Q6P3C4 mus musculus
90	78	12.4	242	2	Q607I7	Q607I7 canis famil
91	78	12.4	297	1	Y622TREA	Y622TREA treponema p
92	77.5	12.3	77	2	Q9ZNT5	Q9ZNT5 eichhornia
93	77	12.2	77	1	MT2_VICFA	Q41657 vicia faba
94	77	12.2	77	2	Q93X22	Q93X22 quercus sub
95	77	12.2	79	1	MT2_CICAR	Q39459 cicor ariet
96	77	12.2	79	2	Q92EVO	Q92EVO fagus sylv
97	77	12.2	118	2	Q9MZB1	Q9MZB1 ovis aries
98	77	12.2	136	2	Q8QCT9	Q8QCT9 oryza sativ
99	77	12.2	136	2	Q8QGE8	Q8QGE8 orf virus.
100	77	12.2	146	1	VEGA_SHEEP	P50412 ovis aries

ALIGNMENTS

RESULT 1
 Q9BMV5
 ID Q9BMV5 PRELIMINARY; PRT; 364 AA.
 AC Q9BMV5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Iris-expressed growth factor short form (Platelet derived growth factor D, isoform 2) (SCDGF-B)
 GN Name=IEGF; Synonyms=PDGFB; ORFNames=UNQ1899;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=iris;
 RX MEDLINE=22103462; PubMed=12107412;
 RA Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W., Bouffard G., Smith D., Peterson K.;
 RA "Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium.";
 RL Mol. Vision 8:185-195(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Eaton D., Foster J., Chui C., Crowley C., Curriel B., Deuel B., Dowd P., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandalen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
 RA "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY027518; AAK20082.1; -;
 DR EMBL; BC030645; AAH30645.1; -;
 DR EMBL; AY359116; AAQ89474.1; -;.

DR PIR; JC7591; JC7591.
 DR HSSP; Q9JJS8; LINT0.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000072; PD growth factor.
 DR InterPro; IPR010916; TONB_Box_N.
 DR Pfam; PF00431; CUB; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS0278; PDGF_2; 1.
 DR PROSITE; PS0430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
 SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
 Query Match 100.0%; Score 631; DB 2; Length 364;
 Best Local Similarity 100.0%; Pred. No. 3.6e-61;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VDLRLNDADKRYCTPRNYSVNIRESLKLAVVFFPRCLLVQRCCGCGCTVNRSC 60
 Db 252 VDLRLNDADKRYCTPRNYSVNIRESLKLAVVFFPRCLLVQRCCGCGCTVNRSC 311
 Qy 61 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPR 113
 Db 312 CNSGKTVKYHEVLQFEFGHIKRRGRKTMALVDIQLDHHRCDCICSSRRPR 364
 RESULT 2
 Q9GZP0
 ID Q9GZP0 PRELIMINARY; PRT; 370 AA.
 AC Q9GZP0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Spinal cord-derived growth factor-B (MSTP036) (Platelet-derived growth factor D) (Iris-expressed growth factor long form)
 GN Name=hSCDGF-B; Synonyms=IEGF, PDGFB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
 RA Hanada T., U-Tai K., Imaki J., Miyata Y.;
 RA "Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/falloskein.";
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S., Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J., Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q., Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
 RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
 RA LaChocelle W.J., Jeffers M., McDonald W.F., Chillaakuru R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C., Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J., Shimkets R.A., Rothberg J.M., Lichtenstein H.S.;
 RA "PDGF D, A Novel Protease-Activated Growth Factor.";
 RL Nat. Cell Biol. 3:517-521(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX PubMed=11331881; DOI=10.1038/35074588;
 RA Bergsten E., Uccella M., Li X., Pietras K., Ostman A., Heldin C.H., Allitalo K., Eriksson U.;
 RA "PDGF-D is a specific, protease-activated ligand for the PDGF beta-receptor.";
 RL Nat. Cell Biol. 3:512-516(2001).

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[5]
RN  SEQUENCE FROM N.A.
RP  TISSUE=iris;
RX  MEDLINE=22103462; PubMed=12107412;
RA  Wistow G., Berstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA  Bouffard G., Smith D., Peterson K.;
RT  "Expressed sequence tag analysis of adult human iris for the NEIBank
RT  Project: steroid-response factors and similarities with retinal
RT  pigment epithelium.";
RL  Mol. Vision 8:185-195(2002).
DR  EMBL; AB033832; BAB18903.1; -
DR  EMBL; AF113216; AAG32827.1; -
DR  EMBL; AF335584; AAK38840.1; -
DR  EMBL; AF336376; AAK56136.1; -
DR  EMBL; AY027517; AAK20081.1; -
DR  PIR; JC7591; JC7591.
DR  HSSP; O9JJS8; 1NTO.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0008083; F:growth factor activity; IEA.
DR  GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR  InterPro; IPR000859; CUB.
DR  InterPro; IPR000072; PD growth factor.
DR  InterPro; IPR010916; TONB_Box_N.
DR  Pfam; PF00431; CUB; 1.
DR  SMART; SM00042; CUB; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PS01180; CUB; 1.
DR  PROSITE; PS0278; PDGF; 1.
DR  PROSITE; PS00430; TONB_DEPENDENT_REC.1; UNKNOWN 1.
DR  PROSITE; PS00430; TONB_DEPENDENT_REC.1; UNKNOWN 1.
SQ  SEQUENCE 370 AA; 42848 MW; D387F465E7BB7674 CRC64;

Query Match      100.0%; Score 631; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.7e-61;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 VLDRLNDADKYSCTPRNYSNIREELKLANVFPFRCCLLVQRCGNGCGCTVWNRST 60
DB  258 VLDRLNDADKYSCTPRNYSNIREELKLANVFPFRCCLLVQRCGNGCGCTVWNRST 317
QY  61 CNSGKTVKKYHVELOPEPGHKKRRGAKTMALVDIQDHHRCDCICSSRRP 113
DB  318 CNSGKTVKKYHVELOPEPGHKKRRGAKTMALVDIQDHHRCDCICSSRRP 370

RESULT 3
Q92517 PRELIMINARY; PRT; 370 AA.
ID  Q92517 O9D1L6;
AC  Q92517; O9D1L6;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Platelet-derived growth factor D (Mus musculus 18-day embryo whole
DE  body cDNA, RIKEN full-length enriched library, clone:1110003109
DE  product:platelet-derived growth factor D).
GN  Name=PDGfd;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN=BALB/c;
RX  MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA  LeRochele W.J., Jeffers M., McDonald W.F., Chillaakuru R.A.,
RA  Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA  Burgess C.E., Fernandez E., Degler L.L., Rittman B., Shinkets J.,
RA  Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT  "PDGF D, A Novel Protease-Activated Growth Factor.";
RL  Nat. Cell Biol. 3:517-521(2001).
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=whole body;
RX  MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

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RA  Carninci P., Hayashizaki Y.;
RT  "High-efficiency full-length cDNA cloning.";
RL  Meth. Enzymol. 303:19-44(1999).
[3]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1038/35055500;
RX  MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA  RIKEN FANTOM Consortium;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
[4]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=whole body;
RA  The FANTOM Consortium,
RA  the RIKEN Genome Exploration Research Group Phase I & II Team;
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs.";
RL  Nature 420:563-573(2002).
[5]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=whole body;
RX  MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA  Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT  "Normalization and subtraction of cap-trapper-selected cDNAs to
RT  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL  Genome Res. 10:1617-1630(2000).
[6]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1101/gr.152600;
RX  MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA  Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA  Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
RA  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT  "RIKEN integrated sequence analysis (RISA) system-384-format
RT  sequencing pipeline with 384 multicapillary sequencer.";
RL  Genome Res. 10:1757-1771(2000).
[7]
RN  SEQUENCE FROM N.A.
RP  STRAIN=C57BL/6J; TISSUE=whole body;
RA  Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA  Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA  Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA  Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA  Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA  Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA  Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA  Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA  Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA  Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA  Muramatsu M., Hayashizaki Y.;
RL  Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF335583; AAK38839.1; -
DR  EMBL; AK003359; BAB2735.2; -
DR  HSSP; O9JJS8; 1NTO.
DR  MGD; MGI:1919035; Pdgd.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR  Pfam; PF00431; CUB; 1.
DR  SMART; SM00042; CUB; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PS01180; CUB; 1.
DR  PROSITE; PS0278; PDGF; 1.
SQ  SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;

Query Match      93.2%; Score 588; DB 2; Length 370;
Best Local Similarity 90.3%; Pred. No. 2e-56;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY 1 VDLRLNDADKRYSTPRNYSVNIREEELKLANVVFPPRCLLVQRCGCGGVNWRSC 60
D 258 VDLRLNDVVKYSCYTPRNSVNIREEELKLTNAVFPFRCLLVQRCGCGGVNWKSC 317
QY 61 CNSGKTVKYYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
D 318 CSSGKTVKYYHEVLKFEFGHFKRRGKAKNMALVDIQLDHHRCDCICSSRPPR 370

RESULT 4
Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=rSGDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/bbrc.2000.4187;
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular cloning of SGDGF-B, a novel growth factor homologous to
RT SGDGF/PDGF-C/fallotectin.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
DR EMBL; AB052170; BAB18920.1; -.
DR PIR; JC7592; JC7592.
DR HSP; O9UCV4; INZ1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7B58A251F679BF73 CRC64;

Query Match 92.7%; Score 585; DB 2; Length 370;
Best Local Similarity 89.4%; Pred. No. 4.4e-56;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYSTPRNYSVNIREEELKLANVVFPPRCLLVQRCGCGGVNWRSC 60
D 258 VDLRLNDVVKYSCYTPRNSVNIREEELKLTNAVFPFRCLLVQRCGCGGVNWKSC 317
QY 61 CNSGKTVKYYHEVLQFEPGHIKRRGRKTMALVDIQLDHHRCDCICSSRPPR 113
D 318 CSSGKTVKYYHEVLKFEFGHFKRRGKAKNMALVDIQLDHHRCDCICSSRPPR 370

RESULT 5
Q6V9H4 PRELIMINARY; PRT; 300 AA.
AC Q6V9H4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Iris-expressed growth factor (Fragment).
GN Name=PDGFD;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9996;
RN [1]
RP SEQUENCE FROM N.A.
RX Ray S., Wistow G.;
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RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
FT NON_TER 1 300
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 81.0%; Score 511; DB 2; Length 300;
Best Local Similarity 91.9%; Pred. No. 5.1e-48;
Matches 91; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDLRLNDADKRYSTPRNYSVNIREEELKLANVVFPPRCLLVQRCGCGGVNWRSC 60
D 202 VDLRLNDADKRYCTPRNYSVNIREEELKLTNVVFPFRCLLVQRCGCGGVNWKSC 261
QY 61 CNSGKTVKYYHEVLQFEPGHIKRRGRKTMALVDIQLD 99
D 262 CSSGKTVKYYHEVLKFEFGHFKRRNRKAKNMALVDIQLDH 300

RESULT 6
Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Lung;
RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uetela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Betscholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
RT receptor.";
RL Nat. Cell Biol. 2:302-309(2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF244813; AAF80597.1; -.
DR HSP; Q9JUS8; INT0.
DR Genew; HGNC:8801; PDGFC.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
DR Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 50.5%; Score 318.5; DB 2; Length 345;
Best Local Similarity 53.3%; Pred. No. 1e-26;
Matches 57; Conservative 14; Mismatches 33; Indels 3; Gaps 1;
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QY 1 VLDRLNDADKRYSCYTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 236 VDLNLLTEEVRLSYCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEC 295
QY 61 CNSGKTVKYYKHYEVLOPEPGHKKRGRKTMALVDIQLDHHERCDCIC 107
DB 296 CVPSKTVKYYKHYEVLOLRP---KTGVRGLHKS LTDVALEHHEECDCVC 339

RESULT 7
Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Secretary growth factor-like protein fallotelin (Spinal cord-derived
DE growth factor) (Platelet-derived growth factor C) (VEGF-E).
GN Name-hSCDGF; Synonyms=PDGFC; ORNames=UNQ174;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.J., Lee R.K., Lin S.P., Chen Y.H.;
RT Identification of a novel platelet-derived growth factor-like gene,
RT fallotelin, in the human reproductive tract.;
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M101056200;
RA Gilbertson P.D., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived growth factor C (pdGF-C), a novel growth factor that
RT binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiewand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RA effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.
DR EMBL; AF260738; AAK51637.1; -.
DR EMBL; AY358493; AAK88857.1; -.
DR HSSP; Q9JJS8; INT0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
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DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 50.5%; Score 318.5; DB 2; Length 345;
Best Local Similarity 53.3%; Pred. No. 1e-26;
Matches 57; Conservative 14; Mismatches 33; Indels 3; Gaps 1;

QY 1 VLDRLNDADKRYSCYTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 236 VDLNLLTEEVRLSYCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEC 295
QY 61 CNSGKTVKYYKHYEVLOPEPGHKKRGRKTMALVDIQLDHHERCDCIC 107
DB 296 CVPSKTVKYYKHYEVLOLRP---KTGVRGLHKS LTDVALEHHEECDCVC 339

RESULT 8
Q9I946 PRELIMINARY; PRT; 345 AA.
AC Q9I946;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name-SCDGF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Spinal cord;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
CC -I- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB033829; BAB03265.1; -.
DR HSSP; Q9JJS8; INT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 50.0%; Score 315.5; DB 2; Length 345;
Best Local Similarity 52.8%; Pred. No. 2.2e-26;
Matches 57; Conservative 16; Mismatches 30; Indels 5; Gaps 2;

QY 1 VLDRLNDADKRYSCYTPRNYSVNIREELKLANVVFPRCLLVORCGNCGCGTVNWRSC 60
DB 236 VDLNLLKEVRLSYCTPRNFSVIREELKRTDTIFWPLCLLVKRCGNCACCHQNCNEC 295
QY 61 CNSGKTVKYYKHYEVLOPEPGHKKRGRKTMALVDIQLDHHERCDCIC 107
DB 296 CIPTKVTKYYKHYEVLOLRP---RSRGVRLHKS LTDVPLEHHEECDCVC 339
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DR EMBL; AF117608; AAF22516.1; -.
DR EMBL; AF266467; AAK58566.1; -.
DR EMBL; AK033734; BAC28455.1; -.
DR EMBL; AK042767; BAC31358.1; -.
DR EMBL; AK052947; BAC35216.1; -.
DR HSSP; Q9JJS8; INT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. . . ; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . . ; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match 49.4%; Score 311.5; DB 2; Length 345;
Best Local Similarity 52.3%; Pred. No. 6.2e-26;
Matches 56; Conservative 15; Mismatches 33; Indels 3; Gaps 1;

QY 1 VLDRLNDKAKYSCTPRNSVNIIEELKLANVFFPRCLLVORCGNGCGTGVNWRSC 60
Db 236 VLNLLKKEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQ 295
QY 61 CNSGKTVKKYHEVLQPEPGHKRRGRKTMALVDIQLDHHERCDCIC 107
Db 296 CVPRKVTKKYHEVLQLRP---KTGVKGLHKSITDVALEHHEEDCVC 339

RESULT 11
Q8CII9 PRELIMINARY; PRT; 345 AA.
AC Q8CII9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor, c polypeptide.
GN Name=Pdgfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Mullany S.J.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellon N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; BC037696; AAH37696.1; -.
DR HSSP; Q9JJS8; INT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. . . ; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . . ; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;

Query Match 49.4%; Score 311.5; DB 2; Length 345;
Best Local Similarity 52.3%; Pred. No. 6.2e-26;
Matches 56; Conservative 15; Mismatches 33; Indels 3; Gaps 1;

QY 1 VLDRLNDKAKYSCTPRNSVNIIEELKLANVFFPRCLLVORCGNGCGTGVNWRSC 60
Db 236 VLNLLKKEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQ 295
QY 61 CNSGKTVKKYHEVLQPEPGHKRRGRKTMALVDIQLDHHERCDCIC 107
Db 296 CVPRKVTKKYHEVLQLRP---KTGVKGLHKSITDVALEHHEEDCVC 339

RESULT 12
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Platelet-derived growth factor C.
GN Name=Pdgfc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse Pdgfc gene: dynamic expression in embryonic tissues during
RT organogenesis.";
RL Mech. Dev. 96:209-213(2000).
DR EMBL; AF286725; AAF91483.1; -.
DR HSSP; Q9JJS8; INT0.
DR MGD; MGI:1859631; Pdgfc.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; P:platelet-derived growth factor receptor bin. . . ; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . . ; IDA.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
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Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
 RA Pepper M.S., Glanvis A., Sleeman J.P.;
 DR "Characterization of indolinones which preferentially inhibit VEGF-C-
 DR RT and VEGF-D-induced activation of VEGFR-3 rather than VEGFR-2.";
 DR Eur. J. Biochem. 268:5530-5540(2001).
 CC -I- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
 CC EMBL; AY032728; AAK96008.1; -;
 DR HSSP; P01127; IPDG.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0008283; P:cell proliferation; IEA.
 DR GO; GO:0000074; P:regulation of cell cycle; IEA.

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DR  ProDom: PD001629; PD_growth_factor; 1.
DR  SMART: SM00141; PDGF_1.
DR  PROSITE: PS00249; PDGF_1; 1.
DR  PROSITE: PS0278; PDGF_2; 1.
DR  Growth factor; Mitogen.
KW  D7CAEBBA6C9FABB7D CRC64;
SQ  SEQUENCE 326 AA; 37106 MW; 17106 MW;
Query Match 16.5%; Score 104; DB 2; Length 326;
Best Local Similarity 28.7%; Pred. No. 0.0046;
Matches 31; Conservative 16; Mismatches 37; Indels 24; Gaps 5
Qy 6 LNDADKRYGCTPRNYSVNTREEL-KLVNVVFFPRCLLVQRCGNGCGGTWNWSCTCNSG 64
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 IDEEWQTCSPRETCEVASELKGKTTNTFFKPPCVNVFRCGGCC-----NEESVMCMNT 161
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 65 KT---VKKYHEV---LQFPGHKKRGRKTMALVDIQLDHHERCDCI 106
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 162 STSYISKQLFESVPLTSVP-----ELVPVKIAHHGTCKCL 197
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 17	
Q6DC06	
ID	Q6DC06 PRELIMINARY; PRT; 194 AA.
AC	Q6DC06;
DT	25-OCT-2004 (T-EMBLrel. 28, Created)
DT	25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE	Hypothetical protein.
DE	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NCBI TaxID=7955;
OX	

RC
RA
RX
RY
SZ
TJ
VZ
WZ
XX
YY
ZZ

GENOINFORM ROOM N/A.
SIRAIN=singapore local strain; TISSUE=Embryo;
PubMed=7913; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff P.,
Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:20:26 ; Search time 177.723 Seconds
(without alignments)
805.195 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 1994

Sequence: 1 MHRLIFVYTYLCANFCSCRD.....DIQLDHERKDCICSSRRPPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1994	100.0	370	3	Aay96864 SEQ. ID.
2	1994	100.0	370	3	Aab48653 Human gro
3	1994	100.0	370	3	Aay71130 Human Pla
4	1994	100.0	370	4	Aab60888 Human VEG
5	1994	100.0	370	4	Aau00704 Human PDG
6	1994	100.0	370	4	Aau00698 Human FCT
7	1994	100.0	370	4	Aag65601 Human zve
8	1994	100.0	370	4	Aae00999 Human zve
9	1994	100.0	370	5	Aab85529 Human sec
10	1994	100.0	370	5	Aae15819 Human LP8
11	1994	100.0	370	5	Abb79643 Human FCT
12	1994	100.0	370	5	Abg92893 Human VEG
13	1994	100.0	370	5	Aab47891 Human zve
14	1994	100.0	370	5	Abb79588 Human zve
15	1994	100.0	370	5	Abg78502 Human FCT
16	1994	100.0	370	5	Abg76575 Human sec
17	1994	100.0	370	5	Abg64733 Human alb
18	1994	100.0	370	5	Abp51640 Human zve
19	1994	100.0	370	6	Abu72430 Human gro
20	1994	100.0	370	6	Abg76397 Human gro
21	1994	100.0	370	6	Abb80134 PDGF-D. 6
22	1994	100.0	370	6	AbR43944 Human PDG
23	1994	100.0	370	7	Aae38476 Human pla
24	1994	100.0	370	7	Abw02697 Human zve
25	1994	100.0	370	7	Adg47746 Human zve

26	1994	100.0	370	8	ADJ32755 Human zve
27	1994	100.0	370	8	ADL78000 Albumin f
28	1994	100.0	370	8	ADL67182 Human zve
29	1994	100.0	370	8	ADL18360 Human zve
30	1994	100.0	370	8	ADM57643 Human FCT
31	1994	100.0	370	8	ADO20113 Human PRO
32	1994	100.0	370	8	ADR31427 Human Pla
33	1994	100.0	370	5	AAE15845 Human LP8
34	1989	99.7	370	5	AAE15849 Human LP8
35	1988	99.7	370	4	AAE15847 Human sec
36	1988	99.7	370	5	AAE15847 Human LP8
37	1988	99.7	370	5	AAE15844 Human LP8
38	1988	99.7	370	5	AAE15846 Human LP8
39	1988	99.7	370	5	AAE15851 Human LP8
40	1988	99.7	370	5	ABG76593 Human sec
41	1988	99.7	370	5	ABG64732 Human alb
42	1988	99.7	370	8	ADL77999 Albumin f
43	1986	99.6	370	5	AAE15848 Human LP8
44	1985	99.5	370	5	ABG78507 Human FCT
45	1984	99.5	370	5	AAE15850 Human LP8
46	1982	99.4	368	7	ADG65193 Cell prol
47	1949	97.7	364	4	AAU12264 Human PRO
48	1949	97.7	364	5	AAE15820 Human LP8
49	1949	97.7	364	5	ABB84373 Human PRO
50	1949	97.7	364	5	ABB95579 Human ang
51	1949	97.7	364	6	ABO17708 Novel hum
52	1949	97.7	364	6	ABU80962 Human PRO
53	1949	97.7	364	6	ABU66662 Human PRO
54	1949	97.7	364	6	ABU59743 Novel sec
55	1949	97.7	364	6	ABO24933 Human sec
56	1949	97.7	364	6	ABU66938 Human sec
57	1949	97.7	364	6	ADA45705 Novel hum
58	1949	97.7	364	6	ADA76136 Human PRO
59	1949	97.7	364	6	ADA18786 Human PRO
60	1949	97.7	364	6	ADA61409 Homo sapi
61	1949	97.7	364	6	ADB19194 Novel hum
62	1949	97.7	364	6	ADB27735 Human PRO
63	1949	97.7	364	6	ADA86214 Novel hum
64	1949	97.7	364	6	ADB15778 Human PRO
65	1949	97.7	364	6	ADA47564 Human PRO
66	1949	97.7	364	6	ADA67359 Human PRO
67	1949	97.7	364	6	ADB30366 Human PRO
68	1949	97.7	364	6	ADA85662 Novel hum
69	1949	97.7	364	6	ADA96874 Human PRO
70	1949	97.7	364	6	ADA79178 Human PRO
71	1949	97.7	364	6	ADA87317 Novel hum
72	1949	97.7	364	6	ADB16519 Human PRO
73	1949	97.7	364	6	ADA91611 Novel hum
74	1949	97.7	364	6	ADB14674 Human PRO
75	1949	97.7	364	6	ADB18635 Novel hum
76	1949	97.7	364	6	ADA93850 Human PRO
77	1949	97.7	364	6	ADB19746 Novel hum
78	1949	97.7	364	6	ADB13058 Human PRO
79	1949	97.7	364	6	ABO43241 Novel hum
80	1949	97.7	364	6	ADA74312 Human PRO
81	1949	97.7	364	6	ADA24545 Human PRO
82	1949	97.7	364	6	ADA82069 Human PRO
83	1949	97.7	364	6	ADA75032 Human PRO
84	1949	97.7	364	6	ADA85110 Novel hum
85	1949	97.7	364	6	ADA84558 Novel hum
86	1949	97.7	364	6	ADB29814 Human PRO
87	1949	97.7	364	6	ADA80342 Human PRO
88	1949	97.7	364	6	ADA75584 Human PRO
89	1949	97.7	364	6	ADA46809 Human PRO
90	1949	97.7	364	6	ADB25105 Human PRO
91	1949	97.7	364	6	ADA93281 Human PRO
92	1949	97.7	364	6	ADB26631 Human PRO
93	1949	97.7	364	6	ADB30918 Human PRO
94	1949	97.7	364	6	ADA60846 Homo sapi
95	1949	97.7	364	6	ADB23993 Human PRO
96	1949	97.7	364	6	ADA96322 Human PRO
97	1949	97.7	364	6	ADA80894 Human PRO
98	1949	97.7	364	6	ADA95770 Human PRO

PT Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
XX Alzheimer's disease.

Claim 1; Page 110-111; 143pp; English.

CC The invention relates to the human growth factor homologue zvegfa
CC (AA84853), and nucleic acids encoding it (AAC81555). Zvegfa is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zvegfa has a growth factor domain (AA84854)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AA84855) which has a beta barrel structure. Zvegfa has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegfa or fragments thereof, particularly human zvegfa/human zveg3
CC fusions; expression constructs and host cells comprising human zveg3
CC nucleic acids; the recombinant expression of human zveg3; an antibody
CC which binds to human zveg3 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg3-derived polypeptide; a method
CC of modulating the proliferation, differentiation, migration or metabolism
CC of bone cells, comprising exposing bone cells to zveg3-derived
CC polypeptides; and a method of detecting a genetic abnormality in the
CC zveg3 gene of a patient. Zveg3 proteins and derived fragments may be
CC used to stimulate tissue development or repair, or cellular
CC differentiation or proliferation. They are particularly used for the
CC treatment or repair of liver damage, and may also be used to modulate
CC neurite growth (e.g., in the treatment of Alzheimer's disease or multiple
CC sclerosis). Due to their osteogenic activity, they may be used in the
CC treatment of periodontal disease and fractures. They may also be used to
CC enhance expansion and mobilisation of haematopoietic stem cells and
CC endothelial precursor stem cells, which may be useful in the treatment of
CC ischaemia, in wound healing, and in the modulation of the immune system.
CC The present sequence represents human zveg3

XX Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRRDETQVKG 60
DB 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRRDETQVKG 60
QY 61 NGVQSPFNSVPRNLLTWRHSQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPFNSVPRNLLTWRHSQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGWCHEKVPPIKSRNTQIKITFKSDDDYFVAKPGFKIYYSLEDFQPAAASE 180
DB 121 ETSITIRGWCHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYSLEDFQPAAASE 180
QY 181 TNWESVTSISGVNSPVSPTDPTLIADALDKIAEFDTVEDLLKYFNESQEDLENNY 240
DB 181 TNWESVTSISGVNSPVSPTDPTLIADALDKIAEFDTVEDLLKYFNESQEDLENNY 240
QY 241 LQTPRYGRGSHDRKSKVDLRNDADAKYSCPTPRNSYNIIEELKLANVFPFRCLLVQ 300
DB 241 LQTPRYGRGSHDRKSKVDLRNDADAKYSCPTPRNSYNIIEELKLANVFPFRCLLVQ 300
QY 301 RCGNGCCGTVNRSTCTNSGKTVKHYEVLPFEPGHIKRRGRKTMALVDQLDHHRC 360
DB 301 RCGNGCCGTVNRSTCTNSGKTVKHYEVLPFEPGHIKRRGRKTMALVDQLDHHRC 360
QY 361 DCICSRPRP 370
DB 361 DCICSRPRP 370

RESULT 3

AAY71130

ID AAY71130 standard; protein; 370 AA.

XX AAY71130;
AC 08-SEP-2000 (first entry)
DT Human Platelet Derived Growth Factor (PDGF)-D protein.
DE
XX Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnary;
KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW proliferative; activator; proliferation; differentiation; motility;
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW atherosclerosis; wound; metastasis.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Domain 52..170
FT /label= CUB domain
FT /note= "Participates in protein-protein or carbohydrate
FT interactions"
FT 254..257
FT /label= Proteolytic site
FT /note= "Dibasic motif"
XX WO200027879-A1.
XX
XX 18-MAY-2000.
XX 10-NOV-1999; 99WO-US026462.
XX 10-NOV-1998; 98US-0107852P.
PR 28-DEC-1998; 98US-0113997P.
PR 26-AUG-1999; 99US-0150604P.
PR 04-OCT-1999; 99US-0157108P.
PR 05-OCT-1999; 99US-0157756P.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
PI Oestman A, Heldin C;
XX WPI; 2000-376495/32.
DR N-PSDB; AAD00738.
XX Novel polynucleotides encoding a novel growth factor of cells expressing
PT a platelet-derived growth factor, useful for diagnostic and therapeutic
PT applications, e.g. concerning cancer.
XX Claim 25; Fig 8; 11pp; English.
PS The present sequence is the complete human platelet derived growth factor
CC (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G.
CC It is derived from human foetal lung lamdagt10 cDNA library. It belongs
CC to the VEGF/PDGF family. It functions as an activator of proliferation,
CC differentiation, growth and motility of cells, that express PDGF-D
CC receptor. This sequence is useful for inhibiting the growth of tumours,
CC that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage
CC for generating an activated truncated form is useful for regulating
CC receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for
CC inhibiting tissue remodelling during the invasion of tumour cells into
CC normal cells. PDGF-D may be used to treat wounds, atherosclerosis,
CC metastasis and migration of smooth muscle cells
XX Sequence 370 AA;
Query Match 100.0%; Score 1994; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRRDETQVKG 60

DB 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRRDETQVKG 60

PA (CURA-) CURAGEN CORP.
XX Shinkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX WPI; 2001-316172/33.
DR N-PSDB; AAS04498.
XX Novel growth factor polypeptides termed as FCTR polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
PS Disclosure; Fig 13; 171pp; English.
XX
CC The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
CC FCTR proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the proteins in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting
CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leucopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, Graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy
XX
SQ Sequence 370 AA;
Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNIHLDLYRDETIQVKG 60
Db 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNIHLDLYRDETIQVKG 60
QY 61 NGYVSPRPNSYPNRLLLTWRLHSQENTRIQLVFDNQGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVSPRPNSYPNRLLLTWRLHSQENTRIQLVFDNQGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGRCWGHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSITIRGRCWGHKEVPPRIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TWVESVTSISGVSNYSPVPTLIADALDKKIAEFDTVEDLLKYFNESQWEDLENNY 240
Db 181 TWVESVTSISGVSNYSPVPTLIADALDKKIAEFDTVEDLLKYFNESQWEDLENNY 240
QY 241 LQTPRYGRSYHDKRSKVDLRDLNDKRYSTCPNYSVNIREEKLANVFPFRCCLLVQ 300
Db 241 LQTPRYGRSYHDKRSKVDLRDLNDKRYSTCPNYSVNIREEKLANVFPFRCCLLVQ 300
QY 301 RCGNGCGCTVNRSTCNSTGKTKYKHYEVLPQEPGHIKRRGRKTMALVDIQLDHERC 360
Db 301 RCGNGCGCTVNRSTCNSTGKTKYKHYEVLPQEPGHIKRRGRKTMALVDIQLDHERC 360
QY 361 DCICSRPPR 370
Db 361 DCICSRPPR 370

RESULT 6

AAU00698

ID AAU00698 standard; protein; 370 AA.

XX

AC AAU00698;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human FCTR1 protein present in clone 30664188.0.99.
XX
KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
KW neoplasia; anaemia; leucopenia; baldness; cardiovascular disorder;
KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
KW inflammatory disorder; Graft versus host disease; coagulation;
KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
KW peripheral neuropathy; acute brain injury.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23 /note= "Signal peptide"
FT Protein 24..370 /note= "Mature FCTR1"
FT Domain 53..167 /note= "CUB domain"
FT Domain 272..306 /note= "PDGF domain"
FT Modified-site 276 /note= "N-linked glycosylation site"
FT Domain 302..365 /note= "Metallothionein domain"
FT Domain 350..362 /note= "PDGF domain"
XX
PN WO200125437-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027671.
XX
PR 07-OCT-1999; 99US-0158083P.
PR 13-OCT-1999; 99US-0159231P.
PR 04-JAN-2000; 2000US-0174485P.
PR 03-MAR-2000; 2000US-0186707P.
PR 10-MAR-2000; 2000US-0188250P.
PR 08-AUG-2000; 2000US-0223879P.
PR 12-SEP-2000; 2000US-00662783.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M;
XX
XX WPI; 2001-316172/33.
DR N-PSDB; AAS04498.
XX
PT Novel growth factor polypeptides termed as FCTR polypeptides, useful for
PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
PT wound healing and neuronal disorders.
XX
PS Claim 1; Fig 1; 171pp; English.
XX
CC The sequence represents a protein related to bone morphogenetic protein-1
CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
CC FCTR proteins are useful for treating or preventing a disorder
CC associated with aberrant expression, aberrant processing, or aberrant
CC physiological interactions of the proteins in a mammal, where the
CC disorder is characterised by insufficient or ineffective growth of a cell
CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
CC associated nucleic acids are useful for both promoting and inhibiting

CC growth of cells and tissues and in treatment of cancer, anaemia,
CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
CC inflammatory disorders, Graft versus host disease, coagulation disorders
CC such as haemophilia, and neural disorders including Parkinson's disease,
CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
CC and epilepsy
XX
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLI FVYTLICANFCSCRDTSATPQSASIKALRNANLRRDES NHLTDL YRRDET IQVG 60
Db 1 MHRLI FVYTLICANFCSCRDTSATPQSASIKALRNANLRRDES NHLTDL YRRDET IQVG 60

Qy 61 NGYVQSPRFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Dy 61 NGYVQSPRFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

Qy 121 ETSTIIIRGWCCHKEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAASE 180
Dy 121 ETSTIIIRGWCCHKEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAASE 180

Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVBDLLKYFPNSQEDLENMY 240
Dy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVBDLLKYFPNSQEDLENMY 240

Qy 241 LDTPRYGRS YHDKRSKVDLRLNDDAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300
Dy 241 LDTPRYGRS YHDKRSKVDLRLNDDAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300

Qy 301 RCGNCGGT VNRSC TNSGKT VKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Dy 301 RCGNCGGT VNRSC TNSGKT VKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Dy 361 DCICSSRPPR 370

RESULT 7
AAG65601
ID AAG65601 standard; protein; 370 AA.

AC AAG65601;

DT 07-JAN-2002 (first entry)

DE Human zveg4 polypeptide.

KW Zveg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;
KW bone cancer; osteonclerosis; bone defect; osteogenesis; osteoporosis;
KW osteopathic; vulnerary; human.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein /note= "secretory peptide"
FT Protein 19..370
FT Protein /note= "mature protein"
FT Domain 52..179
FT Domain /note= "CUB domain"
FT Region 180..257
FT Domain /note= "propeptide-like sequence"
FT Domain 258..370
FT Domain /note= "growth factor domain"

PN W0200157083-A1.
XX
PD 09-AUG-2001.
XX
XX 03-MAY-2000; 2000WO-US012095.
XX
XX 04-FEB-2000; 2000US-0180169P.
PR 31-MAR-2000; 2000US-00540224.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbertson DG, Hart CE;
PI
XX WPI: 2001-611088/70.
DR N-PSDB; AAH47772.
XX
PT Use of zveg4 polypeptide for promoting bone, ligament or cartilage
PT growth in mammal at site of fracture, implant, and bone graft, and for
PT promoting growth or differentiation of osteoblasts, chondrocytes in
PT culture.

Example 2; Page 44-47; 57pp; English.

CC The invention relates to the use of zveg4 polypeptide for promoting
CC bone, ligament or cartilage growth in a mammal, and for promoting
CC proliferation or differentiation of osteoblasts, osteoclasts,
CC chondrocytes or bone marrow stem cells in culture. For promoting
CC cartilage growth, chondrocytes are cultured ex vivo in presence of the
CC zveg4 polypeptide and then placed into mammal where cartilage is to be
CC grown. Zveg4 polypeptide is useful for promoting growth of bone,
CC ligament or cartilage in a mammal at a site of bony defect such as
CC fracture, bone graft, implant or periodontal pocket, in humans and non-
CC human animals such as domestic animals including livestock and companion
CC animals. Zveg4 is used for promoting growth of bone, ligament, or
CC cartilage in conditions of bone defects following therapeutic treatments
CC of bone cancers or other conditions characterized by increased bone loss
CC or decreased bone formation, or elevation of peak bone mass in pre-
CC menopausal woman. It is also useful for healing bone following radiation
CC -induced osteonclerosis, repairing bone defects arising from surgery, and
CC promotion of bone healing in plastic surgery, increasing bone formation
CC during distraction osteogenesis, treating bone injuries including repair
CC of cartilage and ligament and treatment of osteoporosis. The present
CC sequence represents a human zveg4 polypeptide
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLI FVYTLICANFCSCRDTSATPQSASIKALRNANLRRDES NHLTDL YRRDET IQVG 60
Dy 1 MHRLI FVYTLICANFCSCRDTSATPQSASIKALRNANLRRDES NHLTDL YRRDET IQVG 60

Qy 61 NGYVQSPRFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Dy 61 NGYVQSPRFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

Qy 121 ETSTIIIRGWCCHKEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAASE 180
Dy 121 ETSTIIIRGWCCHKEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAASE 180

Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVBDLLKYFPNSQEDLENMY 240
Dy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVBDLLKYFPNSQEDLENMY 240

Qy 241 LDTPRYGRS YHDKRSKVDLRLNDDAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300
Dy 241 LDTPRYGRS YHDKRSKVDLRLNDDAKRYSC TPNYSVNI REELKLANVVFPRCLLVQ 300

Qy 301 RCGNCGGT VNRSC TNSGKT VKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Dy 301 RCGNCGGT VNRSC TNSGKT VKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRRPR 370
 Db 361 DCICSSRRPR 370

RESULT 8
 AA00999
 ID AA00999 standard; protein; 370 AA.
 AC AA00999;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human Zvegf4 protein which forms heteromultimer with Zvegf3 protein.

XX Human; Zvegf3 antagonist; cell proliferation; stellate cell activation;
 KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
 KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
 KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
 KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
 KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
 KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
 KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
 KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
 KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
 KW fibroproliferative disorder; Zvegf4 protein.

XX Homo sapiens.
 XX WO200128586-A1.
 PN
 XX 26-APR-2001.
 XX
 XX 23-OCT-2000; 2000WO-US029270.
 XX
 XX 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 01-AUG-2000; 2000US-022223P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Gilbertson DG;
 PI
 XX WPI; 2001-300278/31.
 DR
 XX Use of zvegf3 antagonist for reducing fibroproliferative disorder of
 PT kidney, liver and bone, reducing extracellular matrix production,
 PT treating fibrosis or reducing stellate cell activation in mammal.
 XX
 PS Disclosure; Page 62-63; 70pp; English.

CC The patent discloses materials and methods for reducing cell
 CC proliferation or extracellular matrix production, treating fibrosis and
 CC reducing stellate cell activation in a mammal. The method comprises
 CC administering a composition containing a Zvegf3 antagonist in combination
 CC with a delivery vehicle. The Zvegf3 is a protein that is structurally
 CC related to platelet-derived growth factor (PDGF) and the vascular
 CC endothelial growth factors (VEGF). The Zvegf3 protein is also designated
 CC as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the
 CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
 CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
 CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1
 CC -antitrypsin deficiency, fibrotic disorders of the kidney such as
 CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
 CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
 CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
 CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
 CC fibrotic disorders of pancreas, fibroproliferative disorders of the
 CC vasculature such as transplant vasculopathy and fibroproliferative
 CC disorders of the bone such as osteopetrosis and hyperostosis. The present
 CC sequence is human Zvegf4 protein which forms a heteromultimer with Zvegf3
 CC protein

XX SQ Sequence 370 AA;
 Query Match 100.0%; Score 1994; DB 4; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPQSASIKALRNANLRDSESNHULTDLYRRDETIVKVG 60
 Db 1 MHRLLFVYTLICANFCSCRDTSATPQSASIKALRNANLRDSESNHULTDLYRRDETIVKVG 60

QY 61 NGYVQSPRPNSYPNLLLTWELHSGENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
 Db 61 NGYVQSPRPNSYPNLLLTWELHSGENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

QY 121 ETSITIRGWCQKHEVPRIKSRNTQIKITFSKDDYFVAKPGFKIYYSLLEDFQPAASE 180
 Db 121 ETSITIRGWCQKHEVPRIKSRNTQIKITFSKDDYFVAKPGFKIYYSLLEDFQPAASE 180

QY 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVDLLKYFNPSQWEDLENNY 240
 Db 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVDLLKYFNPSQWEDLENNY 240

QY 241 LDTPRYGRGSYHDKRSKVDLDRLNDDAKRYSCPTPNYSVINIREELKLANVFFPRCLLVQ 300
 Db 241 LDTPRYGRGSYHDKRSKVDLDRLNDDAKRYSCPTPNYSVINIREELKLANVFFPRCLLVQ 300

QY 301 RCGNGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
 Db 301 RCGNGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY 361 DCICSSRRPR 370
 Db 361 DCICSSRRPR 370

RESULT 9
 AAB85529
 ID AAB85529 standard; protein; 370 AA.
 XX
 AC AAB85529;
 XX
 XX 25-SEP-2001 (first entry)
 DT
 XX Human secreted protein (clone Id HGCNC48) .
 DE
 KW Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; human;
 KW ophthalmological; Gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO200155430-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US001431.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 12-SEP-2000; 2000US-0231968P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX *Rosen CA, Komatsuulis GA, Baker KP, Birse CE, Soppet DR;
 *PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
 PI Fiscella M, Ni J, Ruben SM, Barash SC;
 XX
 XX WPI: 2001-476220/51.
 DR N-PSDB; AAH46939.
 XX
 XX 17 isolated nucleic acid molecules encoding human secreted proteins, used

PT to preventing, treating or ameliorating a medical condition.

XX Claim 11; Page 447-449; 482pp; English.

PS The invention provides novel human secreted proteins and polynucleotides

XX encoding them. The secreted proteins can be expressed by standard

CC recombinant methodology. The secreted proteins and polynucleotides are

CC used to prevent, treat or ameliorate a medical condition in e.g. humans,

CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can

CC also be used in diagnosing a pathological condition. The antibodies to

CC the proteins can also be used in alleviating symptoms associated with the

CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme

CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or

CC treated include autoimmune diseases e.g. rheumatoid arthritis, or

CC hyperproliferative disorders e.g. neoplasms of the breast or liver,

CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders

CC e.g. cerebral ischemia, angioneurosis, nervous system disorders e.g.

CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and

CC ocular disorders e.g. corneal infection. The polypeptides can also be

CC used to aid wound healing and epithelial cell proliferation, to prevent

CC skin aging due to sunburn, to maintain organs before transplantation, for

CC supporting cell culture of primary tissues, to regenerate tissues and in

CC chemotaxis. The polypeptides can also be used as a food additive or

CC preservative to increase or decrease storage capabilities. The present

CC sequence represents a human secreted protein

XX

XX Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 1e-188;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETIQVKG 60

DB 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETIQVKG 60

QY 61 NGYVQSPRFPNSYPRNLLLTWRLHSEOENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

DB 61 NGYVQSPRFPNSYPRNLLLTWRLHSEOENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIRGRWCGHKEVPPRIKSRNTNQIKITPKSDDYFVAKGPKIYYSLLEDFOFAAAASE 180

DB 121 ETSTIIRGRWCGHKEVPPRIKSRNTNQIKITPKSDDYFVAKGPKIYYSLLEDFOFAAAASE 180

QY 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWEDLENMY 240

DB 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWEDLENMY 240

QY 241 LDTPRYGRSYHDKRSKVDLRDLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300

DB 241 LDTPRYGRSYHDKRSKVDLRDLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQ 300

QY 301 RCGNCGCGTVNWRSGCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERC 360

DB 301 RCGNCGCGTVNWRSGCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERC 360

QY 361 DCICSSRPPR 370

DB 361 DCICSSRPPR 370

RESULT 10

AAE15819

ID AAE15819 standard; protein; 370 AA.

XX

AC AAE15819;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human LP85 protein #1.

XX

XX LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnery;

KW osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;

KW

KW MSD; therapy; bone growth; cartilage differentiation; wound healing;

KW neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;

KW sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;

KW muscle loss; immobility; bone density.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

XX Peptide 1..112

XX Protein /label= Signal_peptide

XX 13..370

XX /label= Human_mature_LP85_protein

PN WO200189450-A2.

XX

XX 29-NOV-2001.

XX

XX 08-MAY-2001; 2001WO-US011755.

XX

XX 19-MAY-2000; 2000US-0205424P.

PR 11-JAN-2001; 2001US-0261071P.

PR 11-JAN-2001; 2001US-0261076P.

XX

XX (ELIL) LILLY & CO ELI.

XX

XX Beals JM, Gonzalez-Dewhitt PA, Hammond LJ, Lu J, Na S, Su EW;

PI Witcher DR, Wroblewski VJ;

XX

XX WPI; 2002-083040/11.

DR N-PSDB; AAD15819.

XX

XX Analog of a platelet-derived growth factor homolog, LP85 useful for

PT treating osteoporosis, arthritis, sarcopenia, wounds, has one or more

PT amino acid substitutions which destroy the tripeptidyl sequence of native

PT LP85.

XX

XX Claim 11; Page 109-110; 117pp; English.

PS

XX The present invention relates to LP85, an analogue of platelet-derived

CC growth factor (PDGF) homologue. Sequences of the invention are useful for

CC the manufacture of a medicament for treating musculoskeletal disorder

CC (MSD) which include promoting bone growth, cartilage differentiation and

CC function, wound healing, neuron growth, preventing cartilage degradation

CC or neuronal degeneration. They are useful for treating bone fractures,

CC osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,

CC tissue atrophy, traumatised connective tissues, grafted connective

CC tissue and/or transplanted organs, bone or muscle loss due to

CC malignancy, endocrine disorders and immobility. They are also used for

CC prophylactically increasing or maintaining bone density in a mammal. The

CC present sequence is human LP85 protein

XX

XX Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;

Best Local Similarity 100.0%; Pred. No. 1e-188;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETIQVKG 60

DB 1 MHRILFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLLDLYRDETIQVKG 60

QY 61 NGYVQSPRFPNSYPRNLLLTWRLHSEOENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

DB 61 NGYVQSPRFPNSYPRNLLLTWRLHSEOENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120

QY 121 ETSTIIRGRWCGHKEVPPRIKSRNTNQIKITPKSDDYFVAKGPKIYYSLLEDFOFAAAASE 180

DB 121 ETSTIIRGRWCGHKEVPPRIKSRNTNQIKITPKSDDYFVAKGPKIYYSLLEDFOFAAAASE 180

QY 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWEDLENMY 240

DB 181 TNWESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQWEDLENMY 240

QY 241 LDTPIRGSRSHDRSKVDLRLNDADAKYSCPTPNYSVINREELKLANVFFPRCLLVQ 300
 DB 241 LDTPIRGSRSHDRSKVDLRLNDADAKYSCPTPNYSVINREELKLANVFFPRCLLVQ 300
 QY 301 RCGNCGCGTVNWRSCNKGTVKXKHEVLQFEPGHKRRGRKTMALVDIQLDHHRC 360
 DB 301 RCGNCGCGTVNWRSCNKGTVKXKHEVLQFEPGHKRRGRKTMALVDIQLDHHRC 360
 QY 361 DCICSSRRPR 370
 DB 361 DCICSSRRPR 370

RESULT 11
 ABB79643
 ID ABB79643 standard; protein; 370 AA.
 XX AC ABB79643;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human FCTR1 (platelet derived growth factor D).
 XX KW FCTR1; platelet derived growth factor D; PDGFD; human; Crohn's disease;
 KW inflammatory bowel disease; gene therapy; antiinflammatory; vulnery;
 KW cytostatic; cardiovascular.
 XX OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein /label= signal_peptide
 FT Domain 24..370
 FT Domain 53..167
 FT Domain /note= "CUB domain"
 FT Domain 272..306
 FT Domain /note= "PDGF domain"
 FT Domain 302..365
 FT Domain /note= "metallothionein domain"
 FT Domain 350..362
 FT Domain /note= "PDGF domain"
 XX WO200258716-A2.
 XX 01-AUG-2002.
 XX 06-NOV-2001; 2001WO-US043845.
 XX 06-NOV-2000; 2000US-0246206P.
 XX (CURA-) CURAGEN CORP.
 XX Jeffers M, Shimkets RA, Prayaga S, Boldog FL, Yang M, Burgeas CE;
 PI Fernandes ER, Rittman B, Shimkets JB, Larochele WJ, Lichenstein HS;
 DR WPI; 2002-599742/64.
 DR N-PSDB; ABN84524.
 XX Treating, delaying the onset of, or ameliorating an inflammatory
 PT pathology (e.g. inflammatory bowel disease or Crohn's disease) by
 PT administering to the subject fibroblast growth factors or a combination
 PT of growth factors.
 XX Claim 5; Page 19-21; 196pp; English.
 XX The present sequence is the protein sequence of human growth factor
 CC FCTR1, or platelet derived growth factor D (PDGFD), a secreted protein
 CC that shows homology to human vascular endothelial growth factor E and to
 CC human PDGFs A, B and C. FCTR1 RNA is present in pituitary gland tissues,
 CC uterine microvascular endothelial cells, erythrocytes, thyroid,
 CC small intestine, lymphocytes, adrenal gland and salivary gland. The
 CC invention provides FGFCX and FCTR1 growth factors, polypeptides and

CC deletion variants, and methods of using these to treat, delay the onset
 of, or ameliorate, an inflammatory pathology, especially inflammatory
 CC bowel disease, a disease that occurs in the colon or small intestine, or
 CC Crohn's disease (all claimed). FGFCX and FCTR1 polypeptides and deletion
 CC variants are also useful for treating growth and proliferative diseases
 CC such as cancer, angiotensin, collagen formation, fibrotic and
 CC cardiovascular diseases or diabetic ulcers, and in wound healing. They
 CC can be used in screening and detection methods, chromosome mapping,
 CC tissue typing, predictive medicine, diagnostic assays, prognostic assays,
 CC and pharmacogenomics
 XX SQ Sequence 370 AA;
 SQ Query Match 100.0%; Score 1994; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHRLIFVYTLICANFCSCRDTSATPSASIKALRNANLRRDSENLTLTYRDETIQVK 60
 DB 1 MHRLIFVYTLICANFCSCRDTSATPSASIKALRNANLRRDSENLTLTYRDETIQVK 60
 QY 61 NGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFDNQFGLSEANDICRYDFVEVEDIS 120
 DB 61 NGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFDNQFGLSEANDICRYDFVEVEDIS 120
 QY 121 EFTTIIRGRWCHEKVPRIKSRNTQIKITPKSDDYFVAKPGFKIYYSLLDFQPAASE 180
 DB 121 EFTTIIRGRWCHEKVPRIKSRNTQIKITPKSDDYFVAKPGFKIYYSLLDFQPAASE 180
 QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELKYNFESQEDLENMY 240
 DB 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELKYNFESQEDLENMY 240
 QY 241 LDTPIRGSRSHDRSKVDLRLNDADAKYSCPTPNYSVINREELKLANVFFPRCLLVQ 300
 DB 241 LDTPIRGSRSHDRSKVDLRLNDADAKYSCPTPNYSVINREELKLANVFFPRCLLVQ 300
 QY 301 RCGNCGCGTVNWRSCNKGTVKXKHEVLQFEPGHKRRGRKTMALVDIQLDHHRC 360
 DB 301 RCGNCGCGTVNWRSCNKGTVKXKHEVLQFEPGHKRRGRKTMALVDIQLDHHRC 360
 QY 361 DCICSSRRPR 370
 DB 361 DCICSSRRPR 370

RESULT 12
 ABG92893
 ID ABG92893 standard; protein; 370 AA.
 XX AC ABG92893;
 XX DT 19-NOV-2002 (first entry)
 XX DE Human VEGF-like protein zveg 4.
 XX KW VEGF; vascular endothelial growth factor; zveg 3; human;
 KW chromosome 4q28.3; cell proliferation; differentiation; metabolism;
 KW migration; revascularisation; solid tumour; diabetic retinopathy;
 KW psoriasis; rheumatoid arthritis; cancer; autoimmune disease;
 KW inflammation; myocardial ischaemia; scleroderma; fibrosis;
 KW glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn;
 KW skin grafting; female reproductive tract disorder; chronic liver disease;
 KW circulatory disorder; heart failure; neurodegenerative disease;
 KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
 KW neurite outgrowth.
 XX OS Homo sapiens.
 XX PN US6432673-B1.
 XX PD 13-AUG-2002.
 XX


```
CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
CC marrow stem cells are harvested from a patient prior to culture. The
CC method is therefore useful for treating osteoporosis
XX
XX
SQ Sequence 370 AA;
Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60
DB 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60
QY 61 NGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
DB 61 NGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
DB 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSQWQEDLENMY 240
DB 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSQWQEDLENMY 240
QY 241 LDPTRYGRSYHDKRSKVDLDRNLNDADAKRYSCCTPRNYSVNIREEKLKLANVFFPRCLLVQ 300
DB 241 LDPTRYGRSYHDKRSKVDLDRNLNDADAKRYSCCTPRNYSVNIREEKLKLANVFFPRCLLVQ 300
QY 301 RCGNGCGCTVNRSTCNSGKTVKYYHEVLFQEPGHIKRRGRKTMALVDIQLDHHERC 360
DB 301 RCGNGCGCTVNRSTCNSGKTVKYYHEVLFQEPGHIKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
DB 361 DCICSSRRPR 370
RESULT 14
ABB79588
ID ABB79588 standard; protein; 370 AA.
AC ABB79588;
XX
XX 21-OCT-2002 (first entry)
DE Human zveg4 protein.
XX
KW Zveg4; human; kidney; acute tubular necrosis; nephrotropic;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein /label= Signal_peptide
FT /label= Growth_factor_domain+growth_factor_domain
FT /note= "alternatively comprises residues 24-370, 25-370,
FT 35-370 or 52-370"
FT Domain 180..370
FT /label= Growth_factor_domain
FT Domain 246..370
FT /label= Growth_factor_domain
FT /note= "alternatively comprises residues 250-370 or 258-
FT 370"
XX
XX WO200260467-A2.
XX
XX 08-AUG-2002.
XX
XX 26-OCT-2001; 2001WO-US050155.
```

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XX
PR 30-OCT-2000; 2000US-0244479P.
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX Hart CE, Topouzis S;
XX
XX WPI; 2002-590847/63.
DR N-PSDB; ABN84420.
XX
PT Improving kidney function, or enhancing proliferation or survival of
PT kidney tubule epithelial cells or epithelial cell precursors in a mammal
PT comprises administering a zveg4 protein or zveg4 protein-encoding
PT polynucleotide.
XX
PS Claim 4; Page 38-39; 45pp; English.
XX
CC The present sequence is the protein sequence of human vegf4, a protein
CC which activates the alpha-alpha, alpha-beta and beta-beta forms of the
CC platelet-derived growth factor (PDGF) receptor. Zveg4 is structurally
CC related to PDGF and vascular endothelial growth factor. Structural
CC predictions suggest the polypeptide can form homomultimers or
CC heteromultimers that act on tissues by modulating cell proliferation,
CC migration, differentiation or metabolism. The polypeptide comprises a
CC growth factor domain having a cysteine knot structure, and a CUB domain. A
CC propeptide-like sequence extends from residue 180 to either residue 245,
CC 249 or 257. Zveg4 can thus be prepared in a variety of multimeric forms
CC including zveg4(19-370), zveg4(52-370), zveg4(246-370), zveg4(250-
CC 370) and zveg4(258-370). Expression of zveg4 polynucleotide in cultured
CC mammalian cells results in production of a disulfide-bonded, dimeric
CC protein. Mitogenically active protein is generated upon proteolytic
CC processing to remove the CUB and interdomain regions. An active growth
CC factor domain dimer can be produced directly by expressing a truncated
CC polynucleotide. A claimed method of improving kidney function, or
CC enhancing proliferation or survival of kidney tubule epithelial cells or
CC epithelial cell precursors in a mammal, comprises administering a
CC composition containing a zveg4 protein or zveg4 protein-encoding
CC polynucleotide in combination with a delivery vehicle. The method is
CC especially useful for improving kidney function in a mammal suffering
CC from acute tubular necrosis. The zveg4 protein is preferably a disulfide
CC -bonded dimer of 2 polypeptide chains comprising residues 258-370. 250-
CC 370 or 246-370 of the present sequence, or a disulfide-bonded dimer of 2
CC polypeptide chains, each chain consisting of residues x - y, where the
CC protein is optionally glycosylated, and x is 16, 17, 18, 19, 20, 21, 22,
CC 24, 25, 35, 52, 175, 177, 178, 179, 180, 181, 182, 183, 184, 185,
CC 246, 250, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262 or 263, and y
CC is 365, 366, 367, 369 or 370
XX
SQ Sequence 370 AA;
Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60
DB 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLRYRDETIQVKG 60
QY 61 NGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
DB 61 NGYVQSPFPNSYPNLLLTWRLHSEQENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
DB 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSQWQEDLENMY 240
DB 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSQWQEDLENMY 240
QY 241 LDPTRYGRSYHDKRSKVDLDRNLNDADAKRYSCCTPRNYSVNIREEKLKLANVFFPRCLLVQ 300
DB 241 LDPTRYGRSYHDKRSKVDLDRNLNDADAKRYSCCTPRNYSVNIREEKLKLANVFFPRCLLVQ 300
```

```
QY 301 RCGNCGCGTNNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||||
Db 301 RCGNCGCGTNNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||||
QY 361 DCICSSRPPR 370
    |||||
Db 361 DCICSSRPPR 370
    |||||

RESULT 15
ABG78502
ID ABG78502 standard; protein; 370 AA.
XX
AC ABG78502;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human FCTR 1 protein.
XX
KW 30664188 antigen; blood; cancer; human; FCTR.
XX
OS Homo sapiens.
XX
PN WO200259618-A2.
XX
PD 01-AUG-2002.
XX
PF 16-NOV-2001; 2001WO-US048901.
XX
PR 16-NOV-2000; 2000US-00715332.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M, Andrews D, Larochele W;
XX
DR WPI; 2002-619187/66.
DR N-PSDB; ABS63515.
XX
Detecting presence or amount of 30664188 antigen in a sample, by
PT contacting the biological sample with agent that binds the antigen, and
PT detecting the presence or amount of agent bound to the antigen.
XX
PS Example 1; Page 11-13; 177pp; English.
XX
CC The present invention relates to a new method of detecting the presence
CC of 30664188 antigen in a sample. The invention is useful for detecting
CC the presence of 30664188 in a biological sample (e.g. blood or its
CC component originating from a mammal, preferably human), and for
CC contributing to diagnosis of cancer in a subject. The present amino acid
CC sequence represents a human FCTR protein, as described in the methods of
CC the invention
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNNLTDLRRDETIOVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNNLTDLRRDETIOVKG 60

QY 61 NGYVQSPFPNPNYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNPNYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDIS 120

QY 121 ETSITIIIRGWCCHKVPPRIKSRNQIKITPKSDDYFVAKPGFKIYSLLEDFOFAASE 180
Db 121 ETSITIIIRGWCCHKVPPRIKSRNQIKITPKSDDYFVAKPGFKIYSLLEDFOFAASE 180

QY 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVDDLKLYFNPESWQEDLENNY 240
```

```
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVDDLKLYFNPESWQEDLENNY 240
    |||||
QY 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCPTPNYSVNIRELKLANVVFFPRCLLVQ 300
    |||||
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCPTPNYSVNIRELKLANVVFFPRCLLVQ 300
    |||||
QY 301 RCGNCGCGTNNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||||
Db 301 RCGNCGCGTNNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMALVDIQLDHHERC 360
    |||||
QY 361 DCICSSRPPR 370
    |||||
Db 361 DCICSSRPPR 370
    |||||

RESULT 16
ABG76575
ID ABG76575 standard; protein; 370 AA.
XX
AC ABG76575;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human secreted protein #7.
XX
KW Human; secreted protein; autoimmune disease; blood coagulation disorder;
KW blood platelet disorder; hyperproliferative disorder; renal disorder;
KW neurodegenerative disorder; cardiovascular disorder; vascular disorder;
KW respiratory disorder; endocrine disorder; reproductive disorder;
KW gastrointestinal disorder; infectious disease; antianaemic; cytostatic;
KW antiarthritic; immunosuppressive; antiaesthatic; antidiabetic;
KW antiinflammatory; antipsoriatic; antiparkinsonian; neuroprotective.
XX
OS Homo sapiens.
XX
PN US2002120103-A1.
XX
PD 29-AUG-2002.
XX
PF 27-JUL-2001; 2001US-00915582.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 12-SEP-2000; 2000US-0231968P.
PR 17-JAN-2001; 2001WO-US001431.
XX
PA (ROSE/) ROSEN C A.
PA (KOMA/) KOMATSOULIS G A.
PA (BAKE/) BAKER K P.
PA (BIRS/) BIRSE C E.
PA (SOPP/) SOPPET D R.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIP/) WEI P.
PA (EBNE/) EBNER R.
PA (DUAN/) DUAN D R.
PA (SHIY/) SHI Y.
PA (CHOI/) CHOI G H.
PA (FISC/) FISCELLA M.
PA (NIJJ/) NI J.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
PI Fiscella M, Ni J, Ruben SM, Barash SC;
XX
DR WPI; 2002-608160/65.
DR N-PSDB; ABS58475.
XX
PT New secreted polypeptides and encoding polynucleotides, useful for
PT preventing, treating and diagnosing diseases e.g. anemia, cancer,
```

PT diabetes, aethma, psoriasis, Parkinson's and Alzheimer's.
PS Claim 11; Page 389-390; 238pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule which encodes
CC a human secreted protein. The sequences are useful for diagnosing or
CC diagnosing a susceptibility to a pathological condition in a subject
CC comprising determining the presence or absence of a mutation in the DNA
CC or expression of the protein. The sequences are useful for identifying a
CC binding partner to the protein comprising contacting the protein with a
CC binding partner and determining whether the binding partner effects an
CC activity. The DNA and protein sequences are used for preventing, treating
CC or ameliorating a medical condition such as an autoimmune disease (e.g.
CC multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g.
CC atirbinogenaemia, haemophilia), blood platelet disorders (e.g.
CC thrombocytopenia), hyperproliferative disorders (e.g. sarcoidosis, Sezary
CC syndrome), neurodegenerative disorders (e.g. Alzheimer's disease,
CC Parkinson's disease), renal disorders (e.g. renal vein thrombosis, kidney
CC infarction), cardiovascular disorders (e.g. cardiac arrest,
CC pericarditis), vascular disorders (e.g. aneurysm, ischaemia), respiratory
CC disorders (e.g. tonsillitis, laryngitis), endocrine disorders (e.g.
CC acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea,
CC anorchia), gastrointestinal disorders (e.g. gastroenteritis, pyloric
CC stenosis), infectious diseases (e.g. polio, rubella) and cancer. The
CC Sequences ABG76569-ABG76616 represent human secreted proteins of the
CC invention
XX
XX Sequence 370 AA:
Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETTLQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETTLQVKG 60
QY 61 NGVQSPRPNSYPNRLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Db 61 NGVQSPRPNSYPNRLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
Db 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
QY 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNPESWQEDLENMY 240
Db 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNPESWQEDLENMY 240
QY 241 LOTPRYGRSYHDKRSKVDLDRINDDAKRYSCYCTPRNYSVNIREELKLANVFFPRLVQ 300
Db 241 LOTPRYGRSYHDKRSKVDLDRINDDAKRYSCYCTPRNYSVNIREELKLANVFFPRLVQ 300
QY 301 RCGNGCGCTVNWRSCTNSGKTVKYYHEVLPQEPGHIKRRGRAKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTNSGKTVKYYHEVLPQEPGHIKRRGRAKTMALVDIOLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370
RESULT 17
ABG64733
ID ABG64733 standard; protein; 370 AA.
XX
XX
AC ABG64733;
XX
XX 27-AUG-2002 (First entry)
DT Human albumin fusion protein #1408.
DE Human albumin fusion protein #1408.
XX
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;

KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytostatic; antifertility; antiinflammatory; antitumor;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurologic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200177137-A1.
PD 18-OCT-2001.
PF 12-APR-2001; 2001WO-US011988.
XX
PR 12-APR-2000; 2000US-0229358P.
PR 25-APR-2000; 2000US-0199384P.
PR 21-DEC-2000; 2000US-0256931P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Haeeltline WA;
XX
XX WPI; 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1459-1460; 2102pp; English.
XX
CC The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA, also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or disorder
CC that may be modulated by therapeutic protein X. The albumin extends the
CC shelf-life of protein X, and may increase its biological in vitro/in vivo
CC activity. The protein is useful for treating and diagnosing disorders
CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
XX Sequence 370 AA;
Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETTLQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRDETTLQVKG 60
QY 61 NGVQSPRPNSYPNRLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
Db 61 NGVQSPRPNSYPNRLTLTWLHQSQENTRIQLVFDNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
Db 121 ETSTIIRGRWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
QY 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNPESWQEDLENMY 240
Db 181 TWVESVTSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYNPESWQEDLENMY 240
QY 241 LOTPRYGRSYHDKRSKVDLDRINDDAKRYSCYCTPRNYSVNIREELKLANVFFPRLVQ 300
Db 241 LOTPRYGRSYHDKRSKVDLDRINDDAKRYSCYCTPRNYSVNIREELKLANVFFPRLVQ 300
QY 301 RCGNGCGCTVNWRSCTNSGKTVKYYHEVLPQEPGHIKRRGRAKTMALVDIOLDHHERC 360

Db 301 RCGNCGCGTVNWRSCVTNSGKTVKYEVLQFEGHIKRRGAKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPPR 370
Db 361 DCICSSRRPPR 370

RESULT 18

ABP51640
ID ABP51640 standard; protein; 370 AA.

XX AC ABP51640;
XX 30-SEP-2002 (first entry)
XX Human zvegfg4 protein SEQ ID NO:2.
XX Human; zvegfg4; cell proliferation; extracellular matrix production;
KW fibroproliferative disorder; PDGF-D; platelet derived growth factor;
KW PDGF; vascular endothelial growth factor; VEGF; cytosatic; nephrotropic;
KW hepatotropic; antiinflammatory; osteopatic; antiarthritic; metastasis;
KW prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis;
KW diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrome;
KW chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis;
KW hyperostosis; osteoarthritis.
XX Homo sapiens.
OS
XX US2002064832-A1.
PN 30-MAY-2002.
XX 14-MAR-2001; 2001US-00808972.
PF 03-MAY-1999; 99US-0132250P.
PR 10-NOV-1999; 99US-0164463P.
PR 04-FEB-2000; 2000US-0180169P.
PR 03-MAY-2000; 2000US-0056459S.
PR 26-SEP-2000; 2000US-0235293P.
XX (HART/) HART C E.
PA (TOPO/) TOPOUZIS S.
PA (GILB/) GILBERTSON D G.
XX Hart CE, Topouzis S, Gilbertson DG;
XX WPI; 2002-573696/61.
DR N-PSDB; ABQ73239.

XX Reducing proliferation or extracellular matrix production by a cell in a
PT mammal, useful for treating fibroproliferative disorders of bone, liver
PT and kidney, comprises administering a zvegfg4 antagonist.

PS Example 3; Page 19-20; 34pp; English.

XX The present invention describes a method for reducing proliferation of or
CC extracellular matrix production by a cell in a mammal. The method
CC comprises administering to the mammal a composition comprising a
CC therapeutically effective amount of a zvegfg4 antagonist chosen from anti-
CC zvegfg4 antibodies, inhibitory polynucleotides, inhibitors of zvegfg4
CC activation, and mitogenically inactive, receptor-binding variants of
CC zvegfg4. Zvegfg4 (also called PDGF-D) is a multi-domain protein that is
CC structurally related to platelet derived growth factor (PDGF) and
CC vascular endothelial growth factors (VEGF). Zvegfg4 has cytosatic,
CC nephrotropic, hepatotropic, antiinflammatory, osteopatic and
CC antiarthritic activities. The method is useful for reducing proliferation
CC of mesangial, epithelial, endothelial, smooth muscle, fibroblast,
CC osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells
CC in a mammal, in particular proliferation of prostate tumour cells, and
CC for reducing extracellular matrix production by a cell in a mammal
CC suffering from a fibroproliferative disorder of kidney, bone or liver. In
CC particular it is useful for reducing stellate cell activation. The method

CC is useful for reducing metastasis of prostate cancer cells to bone in a
CC mammal and for treating a fibroproliferative disorder of kidney, liver or
CC bone in a mammal. Fibroproliferative disorders of the kidney include,
CC glomerulonephritis, diabetic glomerulosclerosis, lupus nephritis, renal
CC arteriosclerosis and nephrotic syndrome, disorders of the liver include
CC chronic active hepatitis and many other types of cirrhosis, and disorders
CC of the bone include osteopetrosis, hyperostosis, osteosclerosis,
CC osteoarthritis, and ectopic bone formation in metastatic prostate cancer.
CC The present sequence represents human zvegfg4, which is used in an example
CC from the present invention

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 1994; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 10-188;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLYRRDETIOVKG 60
DB 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLYRRDETIOVKG 60
QY 61 NGYVQSPRFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLERAEENDICRYDFVEVRDIS 120
DB 61 NGYVQSPRFPNSYPRNLLLTWRHLSQENTRIQLVFDNQFGLERAEENDICRYDFVEVRDIS 120
QY 121 ETSTIIIRGWCCHKVEPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
DB 121 ETSTIIIRGWCCHKVEPPRIKSRTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
QY 181 TNWESVTSSISGSVNSPSTVDPTLIADALDKIAEFTVREDLLKYFNPSQEDLENNY 240
DB 181 TNWESVTSSISGSVNSPSTVDPTLIADALDKIAEFTVREDLLKYFNPSQEDLENNY 240
QY 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCCTPRNYSVNIREELKLANVFFPRCLLVQ 300
DB 241 LDTPRYGRSYHDKRSKVDLDRLNDDAKRYSCCTPRNYSVNIREELKLANVFFPRCLLVQ 300
QY 301 RCGNCGCGTVNWRSCVTNSGKTVKYEVLQFEGHIKRRGAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTVNWRSCVTNSGKTVKYEVLQFEGHIKRRGAKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPPR 370
DB 361 DCICSSRRPPR 370

RESULT 19

ABU72430
ID ABU72430 standard; protein; 370 AA.

XX AC ABU72430;

XX 17-JUN-2003 (first entry)

XX Human growth factor homologue ZVEGFa.

XX Human; growth factor homologue; ZVEGF4; proliferation; differentiation;
KW migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW neurite growth; cardiovascular development; limb development;
KW cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
KW autoimmune disease; inflammation; retinopathy; haemangioma;
KW ischaemic event; neuropathy; acute nerve damage; stroke;
KW central nervous system disease; peripheral nervous system disease;
KW chromosome 11q22.3-23.1.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 52..370
FT Region 52..253 /note= "Specifically claimed in claim 7"
FT Region 180..370 /note= "Specifically claimed in claim 7"

FT /note= "Specifically claimed in claim 5"
 250. .370
 FT /note= "Specifically claimed in claim 7"
 250. .370
 FT /note= "Specifically claimed in claim 2"
 258. .370
 FT /note= "Specifically claimed in claim 1"
 258. .370
 XX US6495668.B1.
 XX 17-DEC-2002.
 XX 03-MAY-2000; 2000US-00564595.
 XX 03-MAY-1999; 99US-0132250P.
 PR 10-NOV-1999; 99US-0164463P.
 PR 04-FEB-2000; 2000US-0180169P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 PI WPI: 2003-352153/33.
 DR N-PSDB; AC64109.
 XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
 PT composition as, e.g. therapeutic agents, diagnostic agents, and research
 PT tools and reagents, includes polypeptides from amino acid residues.
 XX
 PS Claim 1; Col 71-72; 67pp; English.
 XX The invention relates to an isolated protein comprising a first
 CC polypeptide disulphide-bonded to a second polypeptide. The first and
 CC second polypeptides are from 113-138 amino acid residues and comprises
 CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
 CC protein stimulates proliferation, differentiation, or migration of
 CC mesenchymal cells and may modulate activities mediated by cell surface
 CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
 CC semaphorin interactions which may be of use in neurite growth,
 CC cardiovascular development, cartilage and limb development, T- and B-cell
 CC functions as well as treating rheumatoid arthritis, various forms of
 CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
 CC ischaemic events, neuropathies, acute nerve damage, central nervous
 CC system diseases and peripheral nervous system diseases including stroke.
 CC The isolated protein is also used for a pharmaceutical composition as
 CC therapeutic agents, diagnostic agents, and research tools and reagents.
 CC It can be used in the study and regulation of cell and tissue
 CC development, as components of cell culture media. The proteins can form
 CC homomultimers or heteromultimers that act on tissues to control organ
 CC development by modulating cell proliferation, migration, differentiation,
 CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
 CC -23.1. The present sequence represents human ZVEGF4
 XX
 SQ Sequence 370 AA;
 Query Match 100.0%; Score 1994; DB 6; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1e-188;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLYRDETIQVKG 60
 DB 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLTDLYRDETIQVKG 60
 QY 61 NGYVQSPFPNSVPNRLTLTLRLHSENTRIOLVFDNQFGLSEAENDICRYDFVEVEDIS 120
 DB 61 NGYVQSPFPNSVPNRLTLTLRLHSENTRIOLVFDNQFGLSEAENDICRYDFVEVEDIS 120
 QY 121 EFTSTIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLEDFQPAASE 180
 DB 121 EFTSTIRGWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLEDFQPAASE 180
 QY 161 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDVDELLKYFNPEMQEDLENMY 240
 DB 161 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDVDELLKYFNPEMQEDLENMY 240

Db 181 TNWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFDVDELLKYFNPEMQEDLENMY 240
 QY 241 LDTPRYGRGSYHDKRSKVDLDRNLDDAKRYSCCTPRNYSVNIREEELKANVFFPRLCLVQ 300
 Db 241 LDTPRYGRGSYHDKRSKVDLDRNLDDAKRYSCCTPRNYSVNIREEELKANVFFPRLCLVQ 300
 QY 301 RCGNCGCGTVMNRSCCTNSGKTVMKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360
 Db 301 RCGNCGCGTVMNRSCCTNSGKTVMKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360
 QY 361 DCICSSRRPR 370
 Db 361 DCICSSRRPR 370
 RESULT 20
 ABG76397
 ID ABG76397 standard; protein; 370 AA.
 XX
 AC ABG76397;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Human growth factor homologue, zvegfg4.
 XX
 KW Human; growth factor homologue; zvegfg4; fibroblast; smooth muscle cell;
 KW cell-surface platelet-derived growth factor alpha receptor; PDGF;
 KW full-thickness skin wound; female reproductive tract; duodenal ulcer;
 KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;
 KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;
 KW chronic active hepatitis; hepatic chronic passive congestion; stroke;
 KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;
 KW portal vein thrombosis; cardiac sclerosis; new vessel formation;
 KW endothelial precursor stem cell; neovascularisation; wound healing;
 KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;
 KW sensory neurite outgrowth; brain disease; head injury; paralysis;
 KW spinal injury; neurodegenerative disease; diabetic retinopathy;
 KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;
 KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;
 KW proliferative vascular disorder; ocular neovascularisation;
 KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;
 KW angiogenesis; nervous system disorder; cycostatic; hepatotropic;
 KW vulnery; tranquiliser; cerebroprotective; neuroprotective; nootropic;
 KW ophthalmological; dermatological; coagulant; cardiant.
 XX
 OS Homo sapiens.
 PN US2002177193-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 02-MAY-2002; 2002US-00139583.
 XX
 PR 07-DEC-1998; 98US-0111173P.
 PR 06-JUL-1999; 99US-0142576P.
 PR 21-OCT-1999; 99US-0161653P.
 PR 12-NOV-1999; 99US-0165255P.
 PR 07-DEC-1999; 99US-00457066.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 XX
 XX WPI: 2003-328485/31.
 DR N-PSDB; ABX93177.
 XX
 PT New isolated zvegfg3 polypeptide, useful for treating cancer, Alzheimer's
 PT disease, Parkinson's disease, chronic active hepatitis, hepatic vein
 PT thrombosis, comprises growth factor domain and CUB domain.
 XX
 XX Disclosure; Page 51-52; 73pp; English.

CC The present invention relates to the isolation of a growth factor
CC homologue referred to as zvegfg3, and the polynucleotide sequence encoding
CC it. The zvegfg3 polypeptide is useful for stimulating the growth of
CC fibroblasts or smooth muscle cells, or for activating a cell-surface
CC platelet-derived growth factor (PDGF) alpha receptor. The zvegfg3
CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful
CC for treating full-thickness skin wounds, female reproductive tract and
CC prolonged bleeding, periodontal disease, damaged liver tissue, and
CC duodenal ulcers. The polypeptide is also useful as an additive in tissue
CC adhesives for promoting revascularisation of healing tissue. The zvegfg3
CC polypeptide is also useful for treating liver damage including damage due
CC to liver disease, chronic active hepatitis, hepatic chronic passive
CC congestion (CPC), central haemorrhagic necrosis (CHN), hepatic vein
CC thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of
CC cirrhosis. The polypeptide is useful for enhancing expansion and
CC mobilisation of endothelial precursor stem cells, creating and
CC stabilising new vessel formation in areas requiring neovascularisation,
CC including areas of ischaemia, organ transplants, wound healing, and
CC tissue grafting. It may be used for treating peripheral neuropathies by
CC increasing spinal cord and sensory neurite outgrowth, and as part of
CC therapeutic treatment for the regeneration of neurite outgrowths
CC following strokes, brain damage caused by head injuries, and paralysis
CC caused by spinal injuries. Application may also be made in treating
CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,
CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung
CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds
CC zvegfg3 is useful for blocking the mitogenic, chemotactic, or angiogenic
CC effects of zvegfg3, and for treating proliferative vascular disorders,
CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,
CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,
CC and diseases of the nervous system. The present sequence represents human
CC zvegfg4
XX

SQ Sequence 370 AA;

Query Match	100.0%;	Score 1994;	DB 6;	Length 370;
Best Local Similarity	100.0%;	Pred. No. 1e-188;		
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Qy	361	DCICSSRRPPR	370	
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Search completed: November 10, 2005, 09:31:31
Job time : 183.723 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:47 ; Search time 45.9627 Seconds
(without alignments)
600.925 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 194

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1994	100.0	370	4	US-09-540-224-2
3	1994	100.0	370	4	US-09-564-595D-2
4	1994	100.0	370	4	US-09-706-968-37
5	1994	100.0	370	4	US-09-808-972-2
6	1994	100.0	370	4	US-09-823-033-5
7	1994	100.0	370	4	US-09-438-046-8
8	1994	100.0	370	4	US-10-139-583-37
9	1994	100.0	370	4	US-10-039-847A-2
10	1742	87.4	322	4	US-09-438-046-6
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12	1737	87.1	370	4	US-09-564-595D-53
13	1737	87.1	370	4	US-09-808-972-4
14	1737	87.1	370	4	US-10-039-847A-4
15	1403	70.4	317	4	US-09-564-595D-56
16	1357.5	68.1	316	4	US-09-564-595D-55
17	1095	54.9	303	4	US-09-564-595D-57
18	1061.5	53.2	302	4	US-09-564-595D-54
19	982	49.2	300	4	US-09-438-046-4
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22	752	37.7	345	4	US-09-706-968-43
23	752	37.7	345	4	US-09-823-033-4
24	752	37.7	345	4	US-10-139-583-43
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35	742.5	37.2	345	4	US-09-468-647A-110	Sequence 110, App
36	742.5	37.2	345	4	US-09-468-647A-130	Sequence 130, App
37	742.5	37.2	345	4	US-10-139-583-2	Sequence 2, Appli
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47	330	16.5	168	4	US-09-468-647A-27	Sequence 27, Appl
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58	187.5	9.4	986	4	US-09-285-385C-19	Sequence 19, Appl
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ALIGNMENTS

RESULT 1

US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673

GENERAL INFORMATION:

; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/09/457,066

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 37

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-457-066-37

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Best Local Similarity 100.0%; Pred. No. 1.2e-197;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 DCICSSRRPPR 370
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RESULT 2

US-09-540-224-2

; Sequence 2, Application US/09540224

; Patent No. 6468543

GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: Hart, Charles E.

; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

; FILE REFERENCE: 00-28

; CURRENT APPLICATION NUMBER: US/09/540,224

; CURRENT APPLICATION NUMBER: US/09/540,224

; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-540-224-2

Query Match 100.0%; Score 1994; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 1.2e-197;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 RCGNCGCGTVNWSCTNSGKTVKXHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Qy 361 DCICSSRRPPR 370
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RESULT 3

US-09-564-595D-2

; Sequence 2, Application US/09564595D

; Patent No. 6495668

GENERAL INFORMATION:

; APPLICANT: Gilbert, Teresa

; APPLICANT: Hart, Charles E.

; APPLICANT: Sheppard, Paul O.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

; FILE REFERENCE: 99-19

; CURRENT APPLICATION NUMBER: US/09/564,595D

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/304,216

; PRIOR FILING DATE: 1999-05-03

; PRIOR APPLICATION NUMBER: US 60/164,463

; PRIOR FILING DATE: 1999-11-10

; PRIOR APPLICATION NUMBER: US 60/180,169

; PRIOR FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-564-595D-2

Query Match

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Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 4

US-09-706-968-37
; Sequence 37, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-37

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MHRLLFVYTLICANFCSRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
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DB 61 NGYVOSPRFPNSYPNLLLTWRLHSGENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
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DB 121 ETSTIIRGWCCHKVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
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DB 181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEFTDVEOLLKYFNPSQWEDLENNY 240
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QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370



RESULT 5

US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROBLASTIC
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
DB 1 MHRLLFVYTLICANFCSRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
QY 61 NGYVOSPRFPNSYPNLLLTWRLHSGENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
DB 61 NGYVOSPRFPNSYPNLLLTWRLHSGENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGWCCHKVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
DB 121 ETSTIIRGWCCHKVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLLEDFQPAASE 180
QY 181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEFTDVEOLLKYFNPSQWEDLENNY 240
DB 181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEFTDVEOLLKYFNPSQWEDLENNY 240
QY 241 LDTPIRGSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIEELKLANVVFPRCLLVQ 300
DB 241 LDTPIRGSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIEELKLANVVFPRCLLVQ 300
QY 301 RCGNCGCGTVNWRCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Db 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370

RESULT 6
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. 6663870
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
| | | | |
Db 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
Qy 61 NGYQSPRPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
| | | | |
Db 61 NGYQSPRPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGRWCGHKVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
| | | | |
Db 121 ETSTIIRGRWCGHKVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240
| | | | |
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSC TPNYSVNI REELKLANVVFPPRCLLVQ 300
| | | | |
Db 241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSC TPNYSVNI REELKLANVVFPPRCLLVQ 300
Qy 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHI KRRGRAKTMALVDIQLDHHERC 360
| | | | |
Db 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHI KRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370

RESULT 7
US-09-438-046-8
; Sequence 8, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-8

Query Match 100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
| | | | |
Db 1 MHRILFVYTLICANFCSCRDTSATPQASIKALRNANLRRDES NHLTDL YRDETIQVKG 60
Qy 61 NGYQSPRPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
| | | | |
Db 61 NGYQSPRPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGRWCGHKVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
| | | | |
Db 121 ETSTIIRGRWCGHKVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLED FQPAASE 180
Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240
| | | | |
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSC TPNYSVNI REELKLANVVFPPRCLLVQ 300
| | | | |
Db 241 LDTPRYGRSYHDKRSKVDLDRNDADAKRYSC TPNYSVNI REELKLANVVFPPRCLLVQ 300
Qy 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHI KRRGRAKTMALVDIQLDHHERC 360
| | | | |
Db 301 RCGNCGCGTVNWRSCNCGTKVKYHEVLQFEPGHI KRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370

RESULT 8
US-10-139-583-37
; Sequence 37, Application US/10139583
; Patent No. 6814965
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066

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; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-37

Query Match      100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLRYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLRYRDETIQVKG 60

Qy 61 NGYVQSPRPNSYPNRLTLTWRLHSGQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNRLTLTWRLHSGQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

Qy 121 ETSTIIRGWCCHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180

Qy 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240

Qy 241 LDTPRYGRSHYDRSKVDLRLNDADAKRYSTCPNYSVINIREELKLANVVFPPRCLLVQ 300
Db 241 LDTPRYGRSHYDRSKVDLRLNDADAKRYSTCPNYSVINIREELKLANVVFPPRCLLVQ 300

Qy 301 RCGNGCGCTVNRWRSCTNSGKTVKXKHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNGCGCTVNRWRSCTNSGKTVKXKHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 9
US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match      100.0%; Score 1994; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLRYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLTDLRYRDETIQVKG 60

Qy 61 NGYVQSPRPNSYPNRLTLTWRLHSGQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNRLTLTWRLHSGQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

Qy 121 ETSTIIRGWCCHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180

Qy 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240
Db 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESQEDLENNY 240

Qy 241 LDTPRYGRSHYDRSKVDLRLNDADAKRYSTCPNYSVINIREELKLANVVFPPRCLLVQ 300
Db 241 LDTPRYGRSHYDRSKVDLRLNDADAKRYSTCPNYSVINIREELKLANVVFPPRCLLVQ 300

Qy 301 RCGNGCGCTVNRWRSCTNSGKTVKXKHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNGCGCTVNRWRSCTNSGKTVKXKHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

US-09-438-046-6
; Sequence 6, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTIN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OBSTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-6

Query Match      87.4%; Score 1742; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-171;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 LYRDETQVKGNGYVQSPRPNSYPNRLTLTWRLHSGQENTRIQLVFDNQFGLBEAENDI 108
Db 1 LYRDETQVKGNGYVQSPRPNSYPNRLTLTWRLHSGQENTRIQLVFDNQFGLBEAENDI 60

Qy 109 CRYDFVEVEDISETSTIIRGWCCHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYYS 168
Db 61 CRYDFVEVEDISETSTIIRGWCCHKEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYYS 120

Qy 169 LLEDQPAASATNWSSTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 228
Db 169 LLEDQPAASATNWSSTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFN 228
```

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; Sequence 53, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-564-595D-53

Query Match      87.1%; Score 1737; DB 4; Length 370;
Best Local Similarity 85.1%; Pred. No. 4.8e-171;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MHRIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
Db 1 MQRVLVLSILLCANFSCYPTDFATPQASIKALRNANLRDESNNHLDLYQREENIQVTS 60

Qy 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Db 61 NGHVQSPRFPNSYPNLLLTWRLRSQEKTRIQLSFDHQFGLAEAEENDICRYDFVEVEVS 120

Qy 121 ETSTIIRGWCCHKKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAASE 180
Db 121 ESSIVRGRWCCHKKEIPRITSRTNOIKITPKSDDYFVAKPGFKIYYSFVEDFOFAAASE 180

Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVDDLKYNFNPESQOEDLENNY 240
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVDDLKYNFNPESQOEDLENNY 240

Qy 241 LDTPRYGRSVYHDKRSKVDLDRNDDAKRYSCYTPRNSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPHYGRSVYHDKRSKVDLDRNDVAKRYSCYTPRNSVNIREEKLANVVFPPRCLLVQ 300

Qy 301 RCGNCGCGTVNWRSCYTNVRSCTNSGKTVKYYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGTVNWRSCYTNVRSCTNSGKTVKYYHEVLKFEFGHFKRRGKAKNMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 13
US-09-808-972-4
; Sequence 4, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
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; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-540-224-4

Query Match      87.1%; Score 1737; DB 4; Length 370;
Best Local Similarity 85.1%; Pred. No. 4.8e-171;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MHRIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
Db 1 MQRVLVLSILLCANFSCYPTDFATPQASIKALRNANLRDESNNHLDLYQREENIQVTS 60

Qy 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAEENDICRYDFVEVEDIS 120
Db 61 NGHVQSPRFPNSYPNLLLTWRLRSQEKTRIQLSFDHQFGLAEAEENDICRYDFVEVEVS 120

Qy 121 ETSTIIRGWCCHKKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAASE 180
Db 121 ESSIVRGRWCCHKKEIPRITSRTNOIKITPKSDDYFVAKPGFKIYYSFVEDFOFAAASE 180

Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVDDLKYNFNPESQOEDLENNY 240
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVDDLKYNFNPESQOEDLENNY 240

Qy 241 LDTPRYGRSVYHDKRSKVDLDRNDDAKRYSCYTPRNSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDTPHYGRSVYHDKRSKVDLDRNDVAKRYSCYTPRNSVNIREEKLANVVFPPRCLLVQ 300

Qy 301 RCGNCGCGTVNWRSCYTNVRSCTNSGKTVKYYHEVLQFEPGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGTVNWRSCYTNVRSCTNSGKTVKYYHEVLKFEFGHFKRRGKAKNMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
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RESULT 12
US-09-564-595D-53
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; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4

Query Match      87.1%; Score 1737; DB 4; Length 370;
Best Local Similarity 85.1%; Pred. No. 4.8e-171;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

QY 1 MHLRFVYTLICANFCSCRDTSATPOSASIKALRNANLRRDES NHLTDL YRDETIOVKG 60
D 1 MQLVLVSLLCANFCSCYPDTTATPQASIKALRNANLRRDES NHLTDL YRQREENIQVTS 60
QY 61 NGYVQSPRPNSYPNLLLTWLRHSEKTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
D 61 NGHVQSPRPNSYPNLLLTWLRHSEKTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
QY 121 ETSITIRGRCWCGHKEVPPRIKSRITQKITFKSDDYFVAKPGFKIYYSLLEDFQPAASE 180
D 121 ESSTVVRGRCWCGHKEIPRITSRITQKITFKSDDYFVAKPGFKIYYSFVDFQPEASE 180
QY 181 TNWESVTSISGVSNPSVPTDPTLIADALOKKIAEFDTVEDLLKYFNPSQWEDLENNY 240
D 181 TNWESVTSISGVSNPSVPTDPTLIADALOKKIAEFDTVEDLLKYFNPSQWEDLENNY 240
QY 241 LDTPYRGSRVHDKSKVDLRLNDADAKRYSCCTPNYSVNIREELKLANVFFPRCLLVQ 300
D 241 LDTPYRGSRVHDKSKVDLRLNDADAKRYSCCTPNYSVNIREELKLANVFFPRCLLVQ 300
QY 301 RCGNCGCGTVMNRSCCTCNKSKTKVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
D 301 RCGNCGCGTVMNRSCCTCNKSKTKVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
D 361 DCICSSRRPR 370

RESULT 15
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: Sheppard, Paul O.
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match      70.4%; Score 1403; DB 4; Length 317;
Best Local Similarity 83.8%; Pred. No. 1.4e-136;
Matches 263; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

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QY 112 DFVEVEDISESTIIRGRCWCGHKEVPPRIKSRITQKITFKSDDYFVAKPGFKIYYSLLE 171
D 61 DFVEVEDISESTIIRGRCWCGHKEVPPRIKSRITQKITFKSDDYFVAKPGFKIYYSLLE 120
QY 172 DFQPAASETNWESVTSISGVSNPSVPTDPTLIADALOKKIAEFDTVEDLLKYFNPS 231
D 121 DFQPAASETNWESVTSISGVSNPSVPTDPTLIADALOKKIAEFDTVEDLLKYFNPS 180
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Qy 351 DIQLDHHERCDCIC 364
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RESULT 16

US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

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Qy 112 DFVEVEDISSETIIRGWCGHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYSL-L 170
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Qy 171 EDFQPAASATNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPE 230
Db 120 PQFTEA---EINWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPE 176
Qy 231 SWQEDLNNMYLDTPRYGRSYHDKSKVVDLRLNDADAKRYSCCTPRNYSVNIREEELKANV 290
Db 177 SWQEDLNNMYLDTPRYGRSYHDKSKVVDLRLNDADAKRYSCCTPRNYSVNIREEELKANV 236
Qy 291 VFFPRCLLVQRCGGNCGCTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALV 350
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RESULT 17

US-09-564-595D-57

; Sequence 57, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

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Best Local Similarity 67.4%; Pred. No. 1e-104;
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Qy 349 LVDIQLDHHERCDCIC 364
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RESULT 18

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; Sequence 54, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:27:37 ; Search time 169.296 Seconds
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Title: US-10-606-055-2

Perfect score: 1994

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1994	100.0	370	9 US-09-808-972-2	Sequence 56, Appl
4	1994	100.0	370	11 US-09-876-813-2	Sequence 2, Appli
5	1994	100.0	370	11 US-09-833-245-1482	Sequence 1482, Ap
6	1994	100.0	370	13 US-10-086-623-8	Sequence 8, Appli
7	1994	100.0	370	13 US-10-139-583-37	Sequence 37, Appl
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15	1994	100.0	370	14 US-10-277-802-56	Sequence 56, Appl
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28	1994	100.0	370	17 US-10-938-375-5	Sequence 5, Appli
29	1994	100.0	370	18 US-10-888-610-5	Sequence 5, Appli
30	1994	100.0	370	18 US-10-794-352-8	Sequence 8, Appli
31	1994	100.0	370	20 US-11-021-088-37	Sequence 37, Appl
32	1994	100.0	370	20 US-11-080-803-2	Sequence 2, Appli
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34	1988	99.7	370	9 US-09-915-582-74	Sequence 74, Appl
35	1988	99.7	370	11 US-09-833-245-1481	Sequence 1481, Ap
36	1988	99.7	370	14 US-10-277-802-74	Sequence 74, Appl
37	1988	99.7	370	17 US-10-896-972-74	Sequence 74, Appl
38	1949	97.7	364	14 US-10-028-072-186	Sequence 186, App
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94	1949	97.7	364	14	US-10-123-909-186	Sequence 186, App
95	1949	97.7	364	14	US-10-123-910-186	Sequence 186, App
96	1949	97.7	364	14	US-10-124-613-186	Sequence 186, App
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98	1949	97.7	364	14	US-10-125-822-186	Sequence 186, App
99	1949	97.7	364	14	US-10-125-924-186	Sequence 186, App
100	1949	97.7	364	14	US-10-140-860-186	Sequence 186, App

ALIGNMENTS

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RESULT 1
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. US2002004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
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RESULT 2
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; Sequence 2, Application US/09808972
; Patent No. US20020064832A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-808-972-2

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RESULT 3
US-09-915-582-56
; Sequence 56, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1

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; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
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US-09-915-582-56

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DB      301 RCGNGCGGTVMNRSCNKGTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370

RESULT 4
US-09-876-813-2
; Sequence 2, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG 2VEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/09/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/09/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-813-2

Query Match      100.0%; Score 1994; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60
DB      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60

QY      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
DB      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

QY      121 ETSTIIRGWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAAASE 180
DB      121 ETSTIIRGWCCHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLDFQPAAASE 180

QY      181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSQOEDLNNY 240
DB      181 TNWESVTSISGVSNPSVPTDPTLIADALDKKIAEFDTVEDLLKYFNPSQOEDLNNY 240

QY      241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVINREELKLANVFFPRCLLVQ 300
DB      241 LDTPRYGRSYHDKRSKVDLRLNDDAKRYSCPTPNYSVINREELKLANVFFPRCLLVQ 300

QY      301 RCGNGCGGTVMNRSCNKGTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB      301 RCGNGCGGTVMNRSCNKGTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360

QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370

RESULT 5
US-09-833-245-1482
; Sequence 1482, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1482
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1482

Query Match      100.0%; Score 1994; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60
DB      1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRDSNHLTDLRYRDETIQVKG 60

QY      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
DB      61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
```

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Db 61 NGYVQSPRPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
QY 121 ETSTIIIRGWCHEVPPIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db 121 ETSTIIIRGWCHEVPPIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
QY 181 TNWESVTSSISGVSYNSPVSVDPTLIADALDKKIAEFTVEDLLKYFNPESWQEDLENMY 240
Db 181 TNWESVTSSISGVSYNSPVSVDPTLIADALDKKIAEFTVEDLLKYFNPESWQEDLENMY 240
QY 241 LDTPIRYGRSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIRREELKLANVVFPRCLLVQ 300
Db 241 LDTPIRYGRSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIRREELKLANVVFPRCLLVQ 300
QY 301 RCGNGCGGTVNNRSCYCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNGCGGTVNNRSCYCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
```

RESULT 6

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US-10-086-623-8
; Sequence 8, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-623-8
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Query Match 100.0%; Score 1994; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
Db 1 MHRLIFFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60

QY 61 NGYVQSPRPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
```

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QY 121 ETSTIIIRGWCHEVPPIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db 121 ETSTIIIRGWCHEVPPIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
QY 181 TNWESVTSSISGVSYNSPVSVDPTLIADALDKKIAEFTVEDLLKYFNPESWQEDLENMY 240
Db 181 TNWESVTSSISGVSYNSPVSVDPTLIADALDKKIAEFTVEDLLKYFNPESWQEDLENMY 240
QY 241 LDTPIRYGRSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIRREELKLANVVFPRCLLVQ 300
Db 241 LDTPIRYGRSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIRREELKLANVVFPRCLLVQ 300
QY 301 RCGNGCGGTVNNRSCYCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGNGCGGTVNNRSCYCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
```

RESULT 7

```
US-10-139-583-37
; Sequence 37, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-37
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Query Match 100.0%; Score 1994; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLIFFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60
Db 1 MHRLIFFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNNHLDLYRRDETIOVKG 60

QY 61 NGYVQSPRPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120

QY 121 ETSTIIIRGWCHEVPPIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db 121 ETSTIIIRGWCHEVPPIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
QY 181 TNWESVTSSISGVSYNSPVSVDPTLIADALDKKIAEFTVEDLLKYFNPESWQEDLENMY 240
Db 181 TNWESVTSSISGVSYNSPVSVDPTLIADALDKKIAEFTVEDLLKYFNPESWQEDLENMY 240
QY 241 LDTPIRYGRSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIRREELKLANVVFPRCLLVQ 300
Db 241 LDTPIRYGRSYHDKRSKVDLDRLNDADAKRYSCYCTPRNYSVNIIRREELKLANVVFPRCLLVQ 300
QY 301 RCGNGCGGTVNNRSCYCTNSGKTVKKYHEVLQFEPFGHIKRRGRKTMALVDIQLDHHERC 360
```

Db 301 RCGNCGGTVNWRSCNCGTKVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 8

US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Publication No. US20020183273A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match 100.0%; Score 1994; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLYRDETTQVKG 60
Db 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLYRDETTQVKG 60
Qy 61 NGVQSPFPNPNYPRNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPFPNPNYPRNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGRWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSIIIRGRWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Qy 181 TWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Db 181 TWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Qy 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Qy 301 RCGNCGGTVNWRSCNCGTKVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHERC 360
Db 301 RCGNCGGTVNWRSCNCGTKVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 9

US-10-260-539-8
; Sequence 8, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: Li, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko

; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES T
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-539-8

Query Match 100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLYRDETTQVKG 60
Db 1 MRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDRSNHLTDLYRDETTQVKG 60
Qy 61 NGVQSPFPNPNYPRNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPFPNPNYPRNLLTWRHLSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGRWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSIIIRGRWCHEKVPPIKRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Qy 181 TWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Db 181 TWESVTSSISGVSNPSVPTDPTLIADALDKKIAEFTDVEDLLKYFNPSQEDLENNY 240
Qy 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Db 241 LDPYRGRSYHDKRSKVDLRLNDDAKRYSCPTPRNYSVNIREEKLANVVFPPRCLLVQ 300
Qy 301 RCGNCGGTVNWRSCNCGTKVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHERC 360
Db 301 RCGNCGGTVNWRSCNCGTKVKKYHEVLQEPGHIKRRGRKTMALVDIQLDHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 10

US-10-264-361-5
; Sequence 5, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361

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; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-361-5

Query Match      100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLLDLYRRDETIQVG 60
Db 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLLDLYRRDETIQVG 60
Qy 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Db 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFNPSWQEDLENNY 240
Db 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFNPSWQEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Qy 301 RCGNGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHERC 360
Db 301 RCGNGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 11
US-10-258-557-2
; Sequence 2, Application US/10258557
; Publication No. US20030100502A1
; GENERAL INFORMATION:
; APPLICANT: Beals, John
; APPLICANT: Gonzalez-DeWhitt, Patricia
; APPLICANT: Hammond, Lisa
; APPLICANT: Lu, Jirong
; APPLICANT: Na, Songqing
; APPLICANT: Su, Eric
; APPLICANT: Witcher, Derrick
; TITLE OF INVENTION: TREATING MUSCULOSKELETAL DISORDERS USING LP85 AND ANALOGS THEREOF
; FILE REFERENCE: X-14392M
; CURRENT APPLICATION NUMBER: US/10/258,557
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-557-2

Query Match      100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLLDLYRRDETIQVG 60
Db 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLLDLYRRDETIQVG 60
Qy 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Db 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFNPSWQEDLENNY 240
Db 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFNPSWQEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Qy 301 RCGNGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHERC 360
Db 301 RCGNGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 12
US-10-226-559-2
; Sequence 2, Application US/10226559
; Publication No. US20030105015A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/10/226,559
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-559-2

Query Match      100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLLDLYRRDETIQVG 60
Db 1 MHRLLFYVTLICANFCSCRDTSATPQSASIKALRNANLRRDESNNHLLDLYRRDETIQVG 60
Qy 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLAEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Db 121 ETSTIIIRGWCHEVPRIKSRNTNQIKITFKSDDYFVAKPGFKIYYSLLLEDFOPAAASE 180
Qy 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFNPSWQEDLENNY 240
Db 181 TNWESVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVDELLKYFNPSWQEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADAKRYSCCTPRNYSVNIREELKLANVVFPRCLLVQ 300
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Db 241 LPTPRGRSYHDKRSKVDLRLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
QY 301 RCGGCGCGTVNWRSTCNKGTVKKYHEVLOPEGHKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGGCGCGTVNWRSTCNKGTVKKYHEVLOPEGHKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 13

US-10-274-638-2
; Sequence 2, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; FILE REFERENCE: 01-30
; CURRENT APPLICATION NUMBER: US/10/274,638
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/346,117
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-638-2

Query Match 100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
QY 61 NGYVQSPFPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240
Db 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240
QY 241 LPTPRGRSYHDKRSKVDLRLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
Db 241 LPTPRGRSYHDKRSKVDLRLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
QY 301 RCGGCGCGTVNWRSTCNKGTVKKYHEVLOPEGHKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGGCGCGTVNWRSTCNKGTVKKYHEVLOPEGHKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 14

US-10-011-364-4
; Sequence 4, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry

; APPLICANT: Jeffers, Michael
; APPLICANT: Shimkets, Richard
; APPLICANT: Pravaga, Sudhirdas
; APPLICANT: Boldog, Ferenc
; APPLICANT: Yang, Weijia
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Rittman, B.
; APPLICANT: Shimkets, Juliette
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth
; FILE REFERENCE: 15966-557A IBD CIP
; CURRENT APPLICATION NUMBER: US/10/011,364
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/246,206
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/992,840
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-364-4

Query Match 100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSESNHLLTDLYRDETIQVKG 60
QY 61 NGYVQSPFPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPNLLLTWRLHSEENTRIQLVFDNQFGLSEAEANDICRYDFVEVEDIS 120
QY 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
Db 121 ETSTIIRGWCCHKEVPPRIKSRNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE 180
QY 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240
Db 181 TNWESVTSSISGVSNPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPSHQEDLENNY 240
QY 241 LPTPRGRSYHDKRSKVDLRLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
Db 241 LPTPRGRSYHDKRSKVDLRLNDADAKRYCTPRNYSVNIIEELKLANVFFPRCLLVQ 300
QY 301 RCGGCGCGTVNWRSTCNKGTVKKYHEVLOPEGHKRRGRKTMALVDIQLDHHERC 360
Db 301 RCGGCGCGTVNWRSTCNKGTVKKYHEVLOPEGHKRRGRKTMALVDIQLDHHERC 360
QY 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 15

US-10-277-802-56
; Sequence 56, Application US/10277802
; Publication No. US20030190707A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/10/277,802
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431

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; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-802-56

Query Match      100.0%; Score 1994; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60

Qy 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120

Qy 121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db 121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180

Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240

Qy 241 LDTPRYGRSYHDKRSKVDLDRNDLNDADAKRYSCCTPRNYSVNIREEKLKLVVFFPRCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLDRNDLNDADAKRYSCCTPRNYSVNIREEKLKLVVFFPRCLLVQ 300

Qy 301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360
Db 301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360

Qy 361 DCICSSRRP 370
Db 361 DCICSSRRP 370

RESULT 16
US-10-246-091-8
; Sequence 8, Application US/10246091
; Publication No. US20030203844A1
; GENERAL INFORMATION:
; APPLICANT: Delfani, Khoumars
; APPLICANT: Janson, Ann Marie
; APPLICANT: Kuhn, Georg
; APPLICANT: Plate, Karlheinz
; APPLICANT: Schnazer, Anne
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: Treatment of Central Nervous System Disorders
; FILE REFERENCE: 21882-504 (PDGF/VEGF)
; CURRENT APPLICATION NUMBER: US/10/246,091
; PRIOR APPLICATION NUMBER: 60/323,381
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/326,044
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-246-091-8

Query Match      100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60

Qy 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120

Qy 121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db 121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180

Qy 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240
Db 181 TNWESVTSISGVSNPSVTDPTLIADALDKKTAEDFTVEDLLKYFNPSQWEDLENNY 240

Qy 241 LDTPRYGRSYHDKRSKVDLDRNDLNDADAKRYSCCTPRNYSVNIREEKLKLVVFFPRCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLDRNDLNDADAKRYSCCTPRNYSVNIREEKLKLVVFFPRCLLVQ 300

Qy 301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360
Db 301 RCGNCGCGTVNWRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERC 360

Qy 361 DCICSSRRP 370
Db 361 DCICSSRRP 370

RESULT 17
US-10-365-095-2
; Sequence 2, Application US/10365095
; Publication No. US20030224488A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Moore, Margaret D.
; APPLICANT: Swiderek, Kristine M.
; APPLICANT: Birks, Carl W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PREPARING DIMERIC GROWTH FACTORS
; FILE REFERENCE: 01-33
; CURRENT APPLICATION NUMBER: US/10/365,095
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 60/355,882
; PRIOR FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-365-095-2

Query Match      100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPQASIKALRNANLRRDESNNHLLTDLRRDETIOVKG 60

Qy 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLGEEAENDICRYDFVEVEDIS 120

Qy 121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
Db 121 ETSTIIIRGWCHEVPPRIKSRNTNQIKITPKSDDYFVAKPGFKIYYSLLEDFOFAAAASE 180
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Db 121 ETSTIIRGWCHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQFPAASE 180
Qy 181 TWNESVTSISGVSYNSPSTPTLIADALDKKIAEFDTVEDLLKYFNPSWQEDLENNY 240
Db 181 TWNESVTSISGVSYNSPSTPTLIADALDKKIAEFDTVEDLLKYFNPSWQEDLENNY 240
Qy 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVFPFRCLLVQ 300
Db 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVFPFRCLLVQ 300
Qy 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 18
US-10-321-962-4
; Sequence 4, Application US/10321962
; Publication No. US20040006015A1
; GENERAL INFORMATION:
; APPLICANT: Boldos, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Fernandes, Elma
; APPLICANT: Jeffers, Michael E.
; APPLICANT: LaRochelelle, William J.
; APPLICANT: Lichenstein, Henry S.
; APPLICANT: Peterson, Jeffrey
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Rittman, Beth
; APPLICANT: Shimkets, Juliette
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Yang, Meijia
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
; FILE REFERENCE: 15966-557A IBD CIP2
; CURRENT APPLICATION NUMBER: US/10/321,962
; CURRENT FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962-4

Query Match 100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLIFVYTLICANFCSCRDTSATPSASIKALRNANLRDSESNHULTDLYRDETTIQVG 60
Db 1 MHRLIFVYTLICANFCSCRDTSATPSASIKALRNANLRDSESNHULTDLYRDETTIQVG 60
Qy 61 NGVQSPFPNSYPNLLLTWRLHSENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPFPNSYPNLLLTWRLHSENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGWCHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQFPAASE 180
Db 121 ETSTIIRGWCHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQFPAASE 180
Qy 181 TWNESVTSISGVSYNSPSTPTLIADALDKKIAEFDTVEDLLKYFNPSWQEDLENNY 240
Db 181 TWNESVTSISGVSYNSPSTPTLIADALDKKIAEFDTVEDLLKYFNPSWQEDLENNY 240
Qy 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVFPFRCLLVQ 300
Db 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVFPFRCLLVQ 300
Qy 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370
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Qy 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370

RESULT 19
US-10-606-055-2
; Sequence 2, Application US/10606055
; Publication No. US20040043027A1
; GENERAL INFORMATION:
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/10/606,055
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US/09/808,972
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-606-055-2

Query Match 100.0%; Score 1994; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.7e-167;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLIFVYTLICANFCSCRDTSATPSASIKALRNANLRDSESNHULTDLYRDETTIQVG 60
Db 1 MHRLIFVYTLICANFCSCRDTSATPSASIKALRNANLRDSESNHULTDLYRDETTIQVG 60
Qy 61 NGVQSPFPNSYPNLLLTWRLHSENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPFPNSYPNLLLTWRLHSENTRIQLVFDNQFGLSEAENDICRYDFVEVEDIS 120
Qy 121 ETSTIIRGWCHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQFPAASE 180
Db 121 ETSTIIRGWCHEKVPPIKSRNTQIKITFKSDDYFVAKPGFKIYYSLLEDQFPAASE 180
Qy 181 TWNESVTSISGVSYNSPSTPTLIADALDKKIAEFDTVEDLLKYFNPSWQEDLENNY 240
Db 181 TWNESVTSISGVSYNSPSTPTLIADALDKKIAEFDTVEDLLKYFNPSWQEDLENNY 240
Qy 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVFPFRCLLVQ 300
Db 241 LOTPRYGRSYHDKRSKVDLDRNLDDAKRYSCPTPRNYSVNIREEKLANVFPFRCLLVQ 300
Qy 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Db 301 RCGNGCGCTVNWRSCTNSGKTVKKYHEVLQFEPGHIKRRGRKTMALVDIOLDHHERC 360
Qy 361 DCICSSRRPR 370
Db 361 DCICSSRRPR 370
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Db 361 DCICSSRRPR 370

RESULT 20

US-10-664-432-5
 ; Sequence 5, Application US/10664432
 ; Publication No. US20040043031A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Gilbertson, Debra G.
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
 ; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
 ; FILE REFERENCE: 00-12
 ; CURRENT APPLICATION NUMBER: US/10/664,432
 ; CURRENT FILING DATE: 2003-09-19
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-664-432-5

Query Match	100.0%;	Score 1994;	DB 15;	Length 370;
Best Local Similarity	100.0%;	Pred. No. 1.7e-167;		
Matches 370;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1	MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQVKG	60
DB 1	MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQVKG	60
QY 61	NGYVQSPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLFEAEENDICRYDFVEVEDIS	120
DB 61	NGYVQSPFPNSYPNLLLTWRLHSQENTRIQLVFDNQFGLFEAEENDICRYDFVEVEDIS	120
QY 121	ETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE	180
DB 121	ETSTIIRGRWCCHKVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLDFQPAASE	180
QY 181	TNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQEDLENNY	240
DB 181	TNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLLKYFNPSQEDLENNY	240
QY 241	LDTPIYRGSRVHDKSKVDLDRLNDADAKRYSCTPNYSVNIREEKLANVVFPPRCLLVQ	300
DB 241	LDTPIYRGSRVHDKSKVDLDRLNDADAKRYSCTPNYSVNIREEKLANVVFPPRCLLVQ	300
QY 301	RCGGNCGCGTVMNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRAKTMALVDIQLDHHERC	360
DB 301	RCGGNCGCGTVMNRSCCTNSGKTVKKYHEVLQFEPFGHIKRRGRAKTMALVDIQLDHHERC	360
QY 361	DCICSSRRPR 370	
DB 361	DCICSSRRPR 370	

Search completed: November 10, 2005, 09:41:02
 Job time : 172.296 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:24:01 ; Search time 39.0683 Seconds
(without alignments)
911.229 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 1994

Sequence: 1 MHRLIFVYTLICANFCSCRD.....DIQLDHERCDCICSSRPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first-100 summaries

Database :

PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1988	99.7	370	2	JC7591
2	1775	89.0	370	2	spinal cord-derive
3	1737	87.1	370	2	platelet-derived g
4	1933	9.7	823	1	procollagen C-endo
5	189.5	9.5	707	2	procollagen C-endo
6	187.5	9.4	730	1	procollagen C-endo
7	187.5	9.4	986	1	procollagen C-endo
8	187.5	9.4	991	2	procollagen C-endo
9	184.5	9.3	3623	2	intrinsic factor-B
10	176	8.8	927	1	A5 antigen precurs
11	174.5	8.8	1057	1	dorsal-ventral pat
12	173	8.7	3623	2	intrinsic factor-B
13	161	8.1	579	2	membrane-type friz
14	156.5	7.8	1524	2	polypeptide - Afri
15	153	7.7	1464	2	development protei
16	149	7.5	1070	2	colloid-BMP-1 like
17	148	7.4	686	1	Ra-reactive factor
18	144	7.2	2403	2	sanko - human
19	143	7.2	699	1	Ra-reactive factor
20	141.5	7.1	767	2	hypothetical prote
21	138.5	6.9	1004	2	oviductin [EC 3.4.
22	137.5	6.9	3871	2	hypothetical prote
23	137	6.9	276	2	TSG-6 homolog PS4
24	136.5	6.8	449	2	procollagen I C-pr
25	136.5	6.8	597	2	metalloproteinase
26	134	6.7	705	1	complement subcomp
27	130.5	6.5	402	2	procollagen I C-pr
28	129	6.5	277	2	hyaluronate-bindin
29	125.5	6.3	533	2	brain-specific CUB

30	123.5	6.2	275	2	JC6506	tumor necrosis fac
31	122.5	6.1	1290	2	A57190	ebnerin precursor
32	122	6.1	321	2	T33161	hypothetical prote
33	121	6.1	419	2	S69207	vascular endotheli
34	120.5	6.0	333	2	T21595	hypothetical prote
35	120	6.0	695	1	S05008	complement subcomp
36	118.5	5.9	1034	1	A53663	enteropeptidase (E
37	116.5	5.8	688	1	CIHUS	complement subcomp
38	116.5	5.8	1594	2	T30549	hensin - rabbit
39	114.5	5.7	1019	1	A56318	enteropeptidase (E
40	114.5	5.7	1035	1	A43090	enteropeptidase (E
41	113	5.7	504	2	S56745	mucin (clone pGM31
42	113	5.7	694	2	JC6554	complement subcomp
43	112	5.6	555	2	T21028	hypothetical prote
44	112	5.6	2083	2	T42721	CRP-ductin-alpha p
45	112	5.6	2197	2	B71600	variant-specific s
46	110.5	5.5	855	2	JC7731	membrane-bound arg
47	109.5	5.5	319	2	IS1569	UVS.2 protein - Af
48	108.5	5.4	463	2	T32037	hypothetical prote
49	108.5	5.4	1830	2	E82909	conserved hypothet
50	107.5	5.4	391	2	T34284	hypothetical prote
51	103.5	5.2	248	2	B83134	probable pili assem
52	103	5.2	386	2	T16099	hypothetical prote
53	103	5.2	434	2	B72410	alkaline phosphata
54	101	5.1	545	2	T18714	hypothetical prote
55	100.5	5.0	148	2	D49530	16K vascular endot
56	100.5	5.0	879	2	T19919	hypothetical prote
57	100	5.0	417	2	T20199	hypothetical prote
58	100	5.0	1119	2	B70126	surface-located me
59	99.5	5.0	266	2	T18292	hypothetical prote
60	99	5.0	347	2	T20618	hypothetical prote
61	99	5.0	414	2	T50019	hypothetical prote
62	99	5.0	792	2	S61335	hemoglobin recepto
63	99	5.0	1355	2	T22552	hypothetical prote
64	99	5.0	2706	2	T28155	variant-specific s
65	98.5	4.9	200	2	IS1551	platelet-derived g
66	98.5	4.9	215	2	S08220	platelet-derived g
67	98.5	4.9	226	2	IS1550	platelet-derived g
68	98.5	4.9	425	2	AB1018	probable type-I se
69	98.5	4.9	473	2	T14873	HLVD secretion pro
70	98	4.9	425	2	T23226	hypothetical prote
71	97.5	4.9	198	2	JS0735	platelet-derived g
72	97.5	4.9	443	2	T24191	hypothetical prote
73	97.5	4.9	2824	2	T22759	hypothetical prote
74	97	4.9	288	2	T33224	hypothetical prote
75	97	4.9	1546	2	G90603	lipoprotein [impor
76	96.5	4.8	308	2	E86840	protein maturation
77	96.5	4.8	400	2	S53937	hypothetical prote
78	96.5	4.8	2135	2	T14602	variant-specific s
79	96	4.8	730	2	S54625	probable membrane
80	95.5	4.8	188	2	JC4680	vascular endotheli
81	95.5	4.8	207	2	JC4679	vascular endotheli
82	95.5	4.8	1850	2	T27864	hypothetical prote
83	95	4.8	382	2	D64309	hypothetical prote
84	95	4.8	436	2	T23345	hypothetical prote
85	95	4.8	971	1	JQ1634	outer capsid prote
86	95	4.8	4688	2	F82885	hypothetical prote
87	94.5	4.7	411	2	S29129	calreticulin precu
88	94.5	4.7	984	1	DJNVCP	DNA-directed DNA p
89	94.5	4.7	986	2	T41809	DNA polymerase orf
90	94.5	4.7	1076	2	T38122	hypothetical prote
91	94	4.7	166	2	JN0248	platelet-derived g
92	93.5	4.7	413	2	T23098	hypothetical prote
93	93.5	4.7	622	2	F97054	Fe-S oxidoreductas
94	93.5	4.7	1150	2	T40395	LIM domain protein
95	93.5	4.7	1320	2	E59092	hypothetical prote
96	93.5	4.7	4836	2	T14346	herc2 protein - mo
97	93	4.7	411	2	D88087	proteins B0454.7 i
98	93	4.7	917	2	T50979	related to tol pro
99	93	4.7	987	2	G86201	hypothetical prote
100	92.5	4.6	412	2	S72579	hypothetical prote


```

Db      121 ESSTVVRGRWCGHKEIPRTSRITNOIKITFKSDYFAKPGFKITYSFEVEDQPEASE 180
      181 TNNESVTSSTSGSYNSPSTDTPTLADALDKIAEDTVEDLLKFNPNESNEDLENNY 240
      181 TNNESVTSSTSGSYNSPSTDTPTLADALDKIAEDTVEDLLKFNPNESNEDLENNY 240
      241 LDPFRGRGRSYHNRKSKVDRLNDADAKRSCPTPRNYSVNIREEKLKLVNFFPRCLLVQ 300
      241 LDPFRGRGRSYHNRKSKVDRLNDADAKRSCPTPRNYSVNIREEKLKLVNFFPRCLLVQ 300
      301 RCGNGCGCGTVMNRSGCTCNSGKTVKKYHEVLQEPGHIKRRGRAKTALVDIQLDHHERC 360
      301 RCGNGCGCGTVMNRSGCTCNSGKTVKKYHEVLQEPGHIKRRGRAKTALVDIQLDHHERC 360
      361 DCTCSSRPPR 370
      361 DCTCSSRPPR 370

```

RESULT 4

```

A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 1-702, EKRPLQPPRRGRPHQKFRVQKRNTPQ' <MOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takehara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994.
A:Title: Bone morphogenetic protein-1 and a mammalian tollold homologue (lmltd) are encoded
A:Reference number: A58788; WUID:95096114; PMID:77988260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TA>
A:Cross-references: GB:L35278; NID:G619423; PIDN:AA41703.1; PID:G619424
C:Genetics:
A:Gene: GDB:BMP1, BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-323/Product: procollagen C-endopeptidase splice form His #status predicted <MAT>
F:323-431/Domain: ascatin homology <AST>
F:432-431/Domain: Ctr/Cls repeat homology <CTR1>
F:435-544/Domain: Ctr/Cls repeat homology <CTR2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: Ctr/Cls repeat homology <CTR3>
F:738-752/Region: histidine-rich
F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:163-319,185-209,332-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,227/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

```

Query Match

```

Best Local Similarity 9.7%; Score 193; DB 1; Length 823;
Matches 71; Conservative 33; Mismatches 89; Indels 54; Gaps 11;

```

```

QY 59 KNGVYQSPRPFPNSYPNNLLTWRLHSQENTRIQLVFNQFGLBEANDICRDPVEVED 118
      597 KNGSITSPQWPKREYPPNNKCIQWLVAFTQYRISLQFD--FFETEGNDVCKRDPFEVRS 653

```

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QY      119 ISETSTIRGRWCGHKEVPRIRKRTNOIKITFKSDYFAKPGFKI-YYSLE----- 171
      654 GLTADSKLHGKFCG-SEKEVITSQYNNMRVEKSDN-TVSKKGFLAHFSPVLEAGDNR 711
      172 -----DFOPAASETNWESVTSSISGSYNSPSTDTPTLADALD 211
      712 SHLSGLELLCPHALVDTPAPSPALSHGDTHATHTHVHCHPCIDACTCGPGLGASRLS 771
      212 KKAIEDTVEDLLKFNPNESNEDLENNYTD-TPRRGRGRSYHNRKSKVDRLNDADAKRY 270
      772 PQPGHLLTVA-----PQ-----EGSYLDFWDTHRG-----DPKPR---RRKSLKTF 810
      271 SCTPRNY 277
      811 SLTPATF 817

```

RESULT 5

```

A:Accession: JC2218
A:Molecule type: mRNA
A:Residues: 1-707 <MAE>
A:Cross-references: UNIPROT:P98070; GB:L12249; NID:G406540; PIDN:AAA16313.1; PID:G40654
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology;
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:23-284/Domain: ascatin homology <AST>
F:285-397/Region: complement 1r/1s-like repeat
F:398-510/Domain: Ctr/Cls repeat homology <CTR1>
F:398-510/Region: complement 1r/1s-like repeat
F:514-550/Domain: Ctr/Cls repeat homology <CTR2>
F:514-550/Region: EGF homology <EGF>
F:554-666/Region: complement 1r/1s-like repeat
F:554-663/Domain: Ctr/Cls repeat homology <CTR3>
F:62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

```

Query Match

```

Best Local Similarity 9.5%; Score 189.5; DB 2; Length 707;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

```

```

QY 59 KNGVYQSPRPFPNSYPNNLLTWRLHSQENTRIQLVFNQFGLBEANDICRDPVEVED 118
      560 KNGSITSPQWPKREYPPNNKCIQWLVAFTQYRISLQFD-QF-ETEGNDVCKRDPFEVRS 616

```

RESULT 6

```

A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, EKRPLQPPRRGRPHQKFRVQKRNTPQ' <MOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takehara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994.
A:Title: Bone morphogenetic protein-1 and a mammalian tollold homologue (lmltd) are encoded
A:Reference number: A37278; WUID:95096114; PMID:77988260
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 703-823 <TA>
A:Cross-references: GB:L35278; NID:G619423; PIDN:AA41703.1; PID:G619424
C:Genetics:
A:Gene: GDB:BMP1, BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; ascatin homology; Ctr/Cls repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-323/Product: procollagen C-endopeptidase splice form His #status predicted <MAT>
F:323-431/Domain: ascatin homology <AST>
F:432-431/Domain: Ctr/Cls repeat homology <CTR1>
F:435-544/Domain: Ctr/Cls repeat homology <CTR2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: Ctr/Cls repeat homology <CTR3>
F:738-752/Region: histidine-rich
F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:163-319,185-209,332-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,227/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

```

A:Molecule type: mRNA
A:Residues: 1-730 <WOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
C:Genetics:
A:Gene: GDB:BMP1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:13-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F:130-730/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:91,142,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.4%; Score 187.5; DB 1; Length 730;
Best Local Similarity 39.4%; Pred. No. 3,3e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 59 KNGVQSPRPNSYPNNLLTWRLHSGENTRIQLVFNQFLBEAENDICRYDVEYED 118
Db 597 KNGSITSPGMEKPEPPNKNCTMQLVAPQYRISIQFD---FFTEGNDVCCYDVEYFS 653
QY 119 ISETSTIIRGWCHEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYY 167
Db 654 GLTADSKLHGKFCG-SEKREVITTSQYNNMVRFEKSDN-TVSKKGFKAHF 700

RESULT 7
B58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
N:Alternate names: bone morphogenic protein 1, tolloid-like splice form
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence__revision 09-Apr-1998 #text_change 09-Jul-2004
C:Accession: A37278; B58788
R:Wozeny, J.M.; Rosen, V.; Celeste, A.U.; Milsosk, L.M.; Witters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRRTPQ' <WOZ>
A:Cross-references: UNIPROT:P13497; GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encod
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: B58788
A:Molecule type: mRNA
A:Residues: 703-986 <TKA>
A:Cross-references: GB:LJ5279; NID:G619860; PIDN:AAQ41710.1; PID:G619861
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>

F:551-587/Domain: EGF homology <EG1>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:707-742/Domain: EGF homology <EG2>
F:747-856/Domain: C1r/C1s repeat homology <C1R4>
F:860-973/Domain: C1r/C1s repeat homology <C1R5>
F:91,142,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.4%; Score 187.5; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 4,8e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 59 KNGVQSPRPNSYPNNLLTWRLHSGENTRIQLVFNQFLBEAENDICRYDVEYED 118
Db 597 KNGSITSPGMEKPEPPNKNCTMQLVAPQYRISIQFD---FFTEGNDVCCYDVEYFS 653
QY 119 ISETSTIIRGWCHEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYY 167
Db 654 GLTADSKLHGKFCG-SEKREVITTSQYNNMVRFEKSDN-TVSKKGFKAHF 700

RESULT 8
I49540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence__revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49540
R:Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A:Reference number: I49540; MUID:94229242; PMID:8174772
A:Accession: I49540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: UNIPROT:P98063; GB:L24755; NID:G439606; PIDN:AAA37306.1; PID:G439607
C:Genetics:
A:Gene: BMP-1
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C:Keywords: hydrolyase; metalloproteinase; zinc
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: C1r/C1s repeat homology <C1R>
F:712-747/Domain: EGF homology <EG2>
F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted

Query Match 9.4%; Score 187.5; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 4,9e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 59 KNGVQSPRPNSYPNNLLTWRLHSGENTRIQLVFNQFLBEAENDICRYDVEYED 118
Db 602 KNGSITSPGMEKPEPPNKNCTMQLVAPQYRISIQFD---FFTEGNDVCCYDVEYFS 658
QY 119 ISETSTIIRGWCHEVPPRIKSRITNOIKITFKSDDYFVAKPGFKIYY 167
Db 659 GLTADSKLHGKFCG-SEKREVITTSQYNNMVRFEKSDN-TVSKKGFKAHF 705

RESULT 9
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence__revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09456
R:Kozrabi, R.; Christiansen, M.; Slihtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3533-3600, 1998
A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.

A:Reference number: 216677; MUID:98241400; PMID:9572993
A:Accession: T09456
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 13633 <KOZ>
A:Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AA082612.1; PID:g3
C:Genetic: 10912
A:Map position: 10912
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>

Query Match 9.3%; Score 184.5; DB 2; Length 3623;

Best Local Similarity 24.3%; Pred. No. 4.4e-05; Matches 85; Conservative 34; Mismatches 120; Indels 11; Gaps 17;

56 IQVKGNGYVSPFPNSYPRLLLTWRLHSQENTRIQLVFPNPGLEAEANDICRYDFVE 115
935 ILTRESTCTIOSPGHPNYPHGINCTWHILVQPNHLILMFET-FHLEFHN--CTNDYLE 991
QY 116 VEDI-SETSTINGRMCGHKEVPPRIKSRNQIKITFKSDDYFAKPGFKIYY----- 167
DB 992 VYDTSETSL--GRYCG-KSIPPSLTSSGNSLMLVFPVDS-DLAGEFLINYEALISAAT 1046
QY 168 SLLEDPQPAASSET-----NMESYSSISGVSYNSPSVDTPLTADALDKIAEF 217
DB 1047 ACLQDYTDGLGTFSPFNPNYNNWECI-----YRI-TVRTGQLIA----- 1087
QY 218 DTVEDLLKYPNPSQWEDLENMVLDTFRYGRSY-----HDKR- 255
DB 1088 -----VHTFNSLEALIGNYTDPLFELIDGGERKPLLGIFGSLNPTIISHSKLM 1140
QY 256 SKVDLRLNDADAKRYSCPTPNYSVINIREELKANVFFPRCLLVQRCGNGCGCTVWMS 315
DB 1141 LKFKSDQI-DTRSGFSAVWDGSGTGC-----CGGN----- 1168
QY 316 CTGNSGCTVKKYHEVLOFEPGHT-----KRGRAKTMALVDIQDHIERC 360
DB 1169 LTTSSGTFISPNYPMFYHSSSECYMWKSSHGSAFLEFKDFLEHHPNC 1218

RESULT 10

A5 antigen precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JH0466; JQ0948
R:Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A>Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology
A:Reference number: JH0466; MUID:91337458; PMID:11908252
A:Accession: JH0466
A:Molecule type: mRNA
A:Residues: 1-927 <TK>
A:Cross-references: GB:J0467; GB:J01077; NID:g222262; PIDN:BA01260.1; PID:g222263
A:Experimental source: tadpole, brain
A>Note: this protein has multiple homologous to complement components C1r and C1s and to C
C:Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology <C1R1>
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-927/Product: A5 antigen #status predicted <A5A>
F:21-18/Domain: C1r/C1s repeat homology <C1R1>
F:147-562/Domain: C1r/C1s repeat homology <C1R2>
F:214-424/Domain: discoidin I amino-terminal homology <DN1>
F:430-584/Domain: discoidin I amino-terminal homology <DN2>
F:646-812/Domain: MAM homology <MAM>
F:861-883/Domain: transmembrane #status predicted <TM>
F:150,261,300,323,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.8%; Score 176; DB 1; Length 927;

Best Local Similarity 27.4%; Pred. No. 3.3e-05; Matches 61; Conservative 35; Mismatches 91; Indels 36; Gaps 9;

4 LIFVYTLICANFSCSDTSTPTQASIGKALRMANLRDESNHLDLYRREPTQVKNQY 63
DB 2 LRLILSCCCWLLTSLSSWAS-----RNDKCG-----DTIKITPSY 38
QY 64 VQSPFPNSYPRLLLTWRLHSQENTRIQLVFPNPGLEAEANDICRYDFVEVEDISET 122
DB 39 LTRAGYPHSTPQRCGEMLIQAEHYORIMINRPHFDLDR-----CKDYVEVIDGDA 95
QY 123 STIIRGMCCHKEVPPRIKSRNQIKITFKSDDYFAKPGFKIYSLLEDPQPAASSETN 182
DB 96 NGQLGKYGCG-KIAPSPVLTGSPSIFLRFVS-DYETPGAGFSIRY---EVFKTGPESCRN 150
QY 183 WESVTSISGVSY--NSPSVDTPL--ADALDKIAEFPTVE 221
DB 151 FTSSNGVSKPKYPEKYPNALBECTYIIFAPKQEIYLFESFE 193

RESULT 11

A39288
dorsal-ventral patterning protein tollold (BC 3.4.24.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A>Title: The Drosophila dorsal-ventral patterning gene tollold is related to human bone
A:Reference number: A39288; MUID:92034970; PMID:1840509
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SH1>
A:Cross-references: UNIPROT:P25723; GB:M76976; NID:g157305; PIDN:AAA8491.1; PID:g15730.
C:Genetic: 1
A:Gene: FlyBase:Flid
A:Cross-references: FlyBase:Fbgn0003719
C:Superfamily: dorsal-ventral patterning protein tollold; aetacrin homology; C1r/C1s rep.
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:116-329/Domain: aetacrin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <C1R1>
F:468-578/Domain: C1r/C1s repeat homology <C1R2>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: C1r/C1s repeat homology <C1R3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: C1r/C1s repeat homology <C1R4>
F:900-1013/Domain: C1r/C1s repeat homology <C1R5>
F:221,225,231,280/Binding site: zinc (His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match 8.8%; Score 174.5; DB 1; Length 1057;

Best Local Similarity 24.2%; Pred. No. 5.1e-05; Matches 84; Conservative 45; Mismatches 115; Indels 103; Gaps 17;

64 VQSPFPNSYPRLLLTWRLHSQENTRIQLVFPNPGLEAEANDICRYDFVEVEDISET 123
DB 480 IDSPNFMIDMPKCEKVMKRTAPDNHQAUKFQS-FELE--KHGCAVDFVEIRDGNHSD 536
QY 124 TIIRGMCCHKEVPPRIKSRNQIKITFKSDDYFAKPGFK----- 164
DB 537 SRLIGRFGCGK-LPPIKIRSNQMYIRFVSDS-SVQKLGSAALMLDVECKFTDHGQH 594
QY 165 IYSLLEDPQPAAS-----ETNMESYSSISGV-----SYNSPSVDT--PTLADAL 210
DB 595 LCLNTLGSYQCCGACVAYELQANGCTCEDACGVDATKSGSYSPSPVVP----- 647
QY 211 DKTIAEFDYVEDLLKYNFNPSEQEDENMVLDTFRYGRSYHPRKSKVD-----LDRLND 266
DB 648 NSQOCVWEVVA-----PNNHVFNLFSIFD--LEGTFHTKCNVYDLIYISKRDV 697
QY 267 AKRYSCPTPNYSVINIREELKANVFFPRCLT-----VQRCG----- 303

Db 698 -----RLKKIGLGYCGHELPVTVNSEQSLRLEFFYSDRTVQSGFVAKFVLIDECGM 749
 Qy 304 GNCG-----GTVNMRCTCNGSGKYVKYHEVLQFPFGHKKRRGAK 345
 Db 750 NNGGCGHRCRNTPFGSIQCGCRANGYTIA-----ENGHNCETBTRCK 788

RESULT 12

T08618
intrinsic factor-B12 receptor CUBILIN precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T08618
J/Moestrup, S.K.; Koziraki, R.; Kristiansen, M.; Kayesen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
A/Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A/Reference number: Z16459; PMID:98148073; PMID:9478979
A/Accession: T08618
A/Status: preliminary;
A/Molecule type: mRNA
A/Residues: 1-3623 <NOE>
A/Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:G3834379; PIDN:AACT1661.1; PID:G3
A/Genetics:
A/Gene: CUBILIN
A/Superfamily: Intrinsic factor-B12 receptor cubilin; EGF homology
C/Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F1-20/Domains: signal sequence #status predicted <SIG>
F121-3623/Product: Intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F133-164/Domains: EGF homology <EGF>
F1436-467/Domains: EGF homology <EGF>

RESULT 13

```

JC7629
membrane-type frizzled-related protein - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7629
R:Katoch, M.
Biochem. Biophys. Res. Commun. 282, 116-123, 2001
A:Title: Molecular cloning and characterization of MFRP, a novel gene encoding a membrane-type frizzled-related protein from human
A:Reference number: JC7629; MUID:21164708; PMID:112633980
A:Accession: JC7629
A:Molecule type: mRNA
A:Residues: 1-579 <KAT>
A:Cross-references: UNIPROT:O9BY79; DBJ:AB055505
C:Comment: This protein, which plays key roles in medulla oblongata as a regulator of th
ubilin domains.
C:Genetics:
A:Gene: mfrp
A:Map position: 11q23
C:Keywords: transmembrane protein

```

	Query Match	8.1%	Score 161;	DB 2;	Length 579;
	Best Local Similarity	26.2%	Pred. No. 0.00024;		
	Matches	49;	Conservative	29;	Mismatches 63; Indels 46; Gaps 9
QY	11 ICANFCGCRDTSATPQASAKIRALRNANLRDESN-----HLTLDYRREDTIQVKG	60			
Db	278 VCDGFANACDGS-----DETNSCAKFGCGGNLTGL-----	308			
QY	61 NGVYGSPFPSPSYPRNILLTWRLHSGENTRIQLVLVDNQFGLAEANDICRYDFVEEDIS	120			
Db	309 QGTSTSEYLOOQYPHQILCTWHISVPAGHSIELQFN--FSLE--AQDECKPFYVEVETS	365			
QY	121 ETSTI-INGRMCGHKNEVPRIKSRNTQIKITFKSDDYFAVAKGFIYSLLEDFO-PAAA	178			
Db	366 SSGAFSLIGRCQG-AEPPPHLVSSHMLAVLFRT-DHGISGGFSATYLAFATENPCGP	423			
QY	179 SETNMES	185			
Db	424 SELSCQA	430			

RESULT 14

T30337
polypeptide - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30337
R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from *Xenopus laevis* oocytes.
A:Reference number: Z20829
A:Accession: T30337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1524 <YAN>
A:Cross-references: UNIPROT: Q91674; EMBL: U081290; NID: S2981640; PDB: G2981641; PDB: AAC2434
C:Superfamily: tryptophan related polypeptide; trypsin homology

RESULT 15

S58984
development protein tolkin (EC 3.4.24.-) - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S58984
R:Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
Genetics 141, 271-281, 1995
A:Title: The tolkin gene is a tolloid/BMP-1 homologue that is essential for *Drosophila* c
A:Reference number: S58984; MUID:96042912; PMID:8536976
A:Accession: S58984
A:Molecule type: mRNA
A:Residues: 1-1464 <PIN>
A:Cross-references: UNIPROT:Q24132; EMBL:U34777; NID:J1002985; PIDN:MAC47015.1; PID:G10G

A>Note: the authors did not translate the codon for residue 722

C:Genetics:

A:Gene: tolkin

A:Cross-references: FlyBase:FBgn004885

C:Keywords: hydrolase; metalloproteinase; zinc

F:529-722/Domain: aetacin homology <AST>

F:958-993/Domain: EGF homology <EGF>

F:118-1153/Domain: EGF homology <EGF>

F:614-618-624-627/Binding site: zinc (His, His, Tyr) #status predicted

F:615/Active site: Glu #status predicted

Query Match

Best Local Similarity 7.7%; Score 153; DB 2; Length 1464;

Matches 57; Conservative 27; Mismatches 60; Indels 86; Gaps 9;

5 IFPTTLCAN-----FCSCRTSATPQASIKALRNANLRDESNHLDYRDETQ 57

1059 VTYYSKLGKGNRLKRICTFCG-----SSIPPTAT-----SESVALRLEFHSKSIQ 1103

58 VKG-----NGY-----63

1104 RSGFAVFPFDIDECANVNGCGHBCRNITGSIYICMCHNGYSMHENGHCKECKEIS 1163

64 ----VQSPRPNSYPRLNLTWRHLSQENTRIQLVFDNQGLEAENDICRYDFVEED 118

1164 APFGTIFSPVDPDYPNACVWHFITTPGHRILKLF--NEFDVSHQE--CTDNNVAVD 1220

119 ISETSTIIRGRWCGHKEVPRIKSRNQIKITKSDDYFAKCGFKIYIS 168

1221 GSESSSVLGRFCGDK-IPPISTSTSNQMYVLTCKN-KQKNGFTASHS 1268

RESULT 16

TJ31069

Colloid-BMP-1 like protein 1 - California sea hare

A:Alternate names: probable metalloproteinase TBL-1

C:Species: Aplysia californica (California sea hare)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: TJ31069

R:Jlu, Q.R.; Hattar, S.; Endo, S.; Macphree, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es

J. Neurosci. 17, 755-764, 1997

A:Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme

A:Reference number: Z20965; MUID:8807484; PMID:8987797

A:Accession: TJ31069

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-1070 <LID>

A:Cross-references: UNIPROT:P91972; EMBL:U57369; NID:91899041; PID:91899042; PIDN:AA0474

C:Superfamily: dorsal-ventral patterning protein tolloid; aetacin homology; C1r/C1s repe

Query Match

Best Local Similarity 7.5%; Score 149; DB 2; Length 1070;

Matches 43; Conservative 34; Mismatches 66; Indels 10; Gaps 7;

61 NGVQSPRPNSYPRLNLTWRHLSQENTRIQLVFDNQGLEAENDICRYDFVEEDIS 120

683 SGITSSPSFDLPPDKNCVWHISAPKGRITLVNFTNMD--LEWRDECDLDPVRRVTVV 740

121 ETSITIRGRWCGHKEVPRIKSRNQIKITKSDDYFAKCGFKIYISLLEDFQPAASE 180

741 GNKRLQGYCGFM-APPSITSLNELRIEFRSD--TLQKTGFSMDY--VADVDECASSN 796

181 TNWSEVTSISGVSYSPTDPTLADALDK 213

797 GGCKHICENTVG-SFHC-SCREGFTLAD-DEK 825

RESULT 17

A59271

Ra-reactive factor (EC 3.4.21.-) 2 precursor - human

N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)

C:Species: Homo sapiens (man)

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C:Accession: A59271

R:Thiel, S.; Vornpu-Jensen, T.; Stover, C.M.; Schwaebble, W.J.; Laursen, S.B.; Poulsen, K

Nature 386, 506-510, 1997

A:Title: A second serine protease associated with mannan-binding lectin that activates

A:Reference number: A59271; MUID:97242412; PMID:9087411

A:Accession: A59271

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-666 <JEN>

A:Cross-references: UNIPROT:O00187; GB:Y09926; NID:94007626; PIDN:CAA11059.1; PID:94007

A:Experimental source: tissue liver

A:Note: Submitted to GenBank, December 1996

A:Note: parts of this sequence, including the amino end of the mature protein, were det

C:Genetics:

A:Gene: MASP2

A:Cross-references: GDB:6071500

A:Map position: 1p36.2-1p36.3

C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homo

C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MNT>

F:19-134/Domain: C1r/C1s repeat homology <C1R1>

F:142-180/Domain: EGF homology <EGF>

F:184-293/Domain: complement factor H repeat homology <C1R2>

F:300-361/Domain: complement factor H repeat homology <FH1>

F:366-430/Domain: complement factor H repeat homology <FH2>

F:445-679/Domain: trypsin homology <TRY>

F:12-90,142-156,152-165,167-180,184-211,241-250,300-348,328-361,366-412,396-430,434-552

F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F:44-445/Cleavage site: Arg-11e (autolytic) #status predicted

F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 7.4%; Score 148; DB 1; Length 686;

Matches 80; Conservative 54; Mismatches 134; Indels 158; Gaps 17;

12 CAN-----FCSCRTSATPQASIKALRNANLRDESNHLDYRDET-----IQV 58

156 CNHHLGFCFCSC-----AGV--LHRKRTCSALCSGOVET 190

59 KNGVQSPRPNSYPRLNLTWRHLSQENTRIQLVFDNQGLEAENDICRYDFVEED 118

191 QRGELSSPEYPRPYKLSCTYSISLEGGFVILDFVESFVETHPTLCYDFUKIQT 250

119 ISETSTIIRGRWCGHKEVPRIKSRNQIKITKSD-----155

251 DRBE-----HGPFCCG-KTLPHRIETKSNVTYITFVDESQDHGCMKIHYSTAHACEYMA 305

156 -----YFAKPGFKIY-----YSLE-----DFQPAASETNWESVTSISGV 194

306 PRNGHVSPOAKYIILKDSIFFCETGYELQGLPLKSTAVCQKGSNDPRPACSIYD 365

195 YNSPSVTDPTLADALDKIAIEF-----DVEDLLKYNEBESQEDLENMYLDTPRYRG 248

366 CGRP-----DLPGRVEXEYITGPVTVYAVAIQY-----SCEETFTYM-----403

249 RSHDRKSKVDLRLNDDAKRSCTPRANSVNIREFKLKLANVFFPRCLLVOR-----301

404 -----KXNDG--KYVCEADGFWTSKGSKSP--VCEVCCGSAFTTGRLY 446

302 -----CGNGCGGV-----NMRSCTCNSGTVKRYHEVLOFEGHILKRG 342

447 GGOKAKPGDFPMQVVLGGTTAGALLYDNNVLTAAHAYEQHDSALDIRNGTILKRLS 506

343 RAKTMA 348

507 PHYTOA 512

RESULT 18

A59386

sanko - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C:Accession: A59386
R:Ranko, S.
submitted to the Protein Sequence Database, March 2001
A:Reference number: A59386
A:Accession: A59386
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-2403 <SASP>
A:Cross-references: UNIPROT:Q9UGM2

Query Match 7.2%; Score 144; DB 2; Length 2403;
Best Local Similarity 22.0%; Pred. No. 0.03;
Matches 72; Conservative 49; Mismatches 112; Indels 94; Gaps 16;

35 NANLRD-----ESNHLT-----DLVRRDRIQVKG-----NGVQSPRPFNRYPRNLL 78
1964 NNNHREDAGVTCGNNHLSPPAPPLNITRPNNTDYSCGGFLSQSPSGDPSFPFGNYPNNAK 2023
QY 79 LTRRLHSEENTRIQLVFNQFGLAEANDI-----CRYDFVEVEDISESTIIRGMCGH 133
DB 2024 CWMDELVQNNRYVYTF-----RVQLEGCGNYIIEVFGPGRYSSPLIARVCDG 2073
QY 134 KEVPRIKSRINOIKITFKSDDYFAKPGFKI-YIS-----LLEDQPPAAASETN 182
DB 2074 AR--GSFTSSNFMISIRFIS-DHSITRRGFRAYEYSSPNDSTNLLCLPNHMQASVRSY 2130
QY 193 WES-----VTSSISGVSYNSPVTDTLTLADALDK-----KLAEDTYE----- 221
DB 2131 LOSLTFASDLVISTWNGYEGCRPQT--PNLVITFTIPYSGCGTFKQADNDTIDYSNFLTA 2189
QY 222 -----DLTKYFNPSWQEDLENNYLDTPRYGRSYHDKRSKVLDRL--NDDA 267
DB 2190 AVSGGIKRRDRLRHVSGRM---LQNTWVDTWYIANDTIHANTIOVEEVOGNPVD 2245
QY 268 K-----RYSCTPRNYSVNIREE 285
DB 2246 NISFYTSSGFYPTVTSRPYVDLNDL 2272

RESULT 19
154763
Ra-reactive factor (EC 3.4.21.-) 1 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: 154763; JN0883
R:Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
Int. Immunol. 6, 665-669, 1994
A:Title: Molecular characterization of a novel serine protease involved in activation of
A:Reference number: 154763; MUID:94289349; PMID:8018603
A:Accession: 154763
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-699 <SASP>
A:Cross-references: UNIPROT:P48740; GB:D28593; NID:G790963; PIDN:BAAO5928.1; PID:G471128
R:Takada, F.; Takayama, Y.; Hattuse, H.; Kawakami, M.
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A:Title: A new member of the C1s family of complement proteins found in a bactericidal F
A:Reference number: JN0883; MUID:94059062; PMID:8240317
A:Accession: JN0883
A:Molecule type: mRNA
A:Residues: 1-224 'E', 236-284, 'G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699 <TAK>
A:Cross-references: DDBJ:D17525; NID:G439712; PIDN:BAAO4477.1; PID:G439713
A:Experimental source: liver
C:Comment: This is a serum bactericidal factor that activates complement C4 and C2 compo
C:Genetics:
A:Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP
A:Cross-references: GDB:361104; GDB:330954; OMIM:600521
A:Map position: 3q27-3q28
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydro
F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
F:19-135/Domain: C1r/C1s repeat homology <C1r1>
F:143-181/Domain: EGF homology <EGF>
F:185-294/Domain: C1r/C1s repeat homology <C1R2>
F:301-362/Domain: complement factor H repeat homology <FH1>
F:367-432/Domain: complement factor H repeat homology <FH2>
F:449-691/Domain: trypsin homology <TRY>
F:49,178,407/Binding site: carbohydrate (asn) (covalent) #status predicted
F:73-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572,
F:159/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted
F:448-449/Cleavage site: Arg-Tile (autolytic) #status predicted
F:490,552,646/Active site: His, Asp, Ser #status predicted

Query Match 7.2%; Score 143; DB 1; Length 699;
Best Local Similarity 19.5%; Pred. No. 0.0071;
Matches 67; Conservative 52; Mismatches 11; Indels 108; Gaps 14;

6 FVYTLICANFGSCRDTSATPOSASIKALRNANLRDESNHLLDLYRRDDETQVKNQVQ 65
156 YCHNYIGCYVCSR-----FGYILHNTNCTCRVCCSDNLF-----TQRTGVIT 198
QY 66 SPRPNYSYPRNLLTLWRHSEENTRIQLVFNQFGLAEANDICRYDFVEVEDISESTI 125
DB 199 SPDFNPYPKSECLYTTLEEGFMVWNLQFEDIDFIDQHEVPYCPDYTKI---KVGPK 254
QY 126 IRGRWCGHKEVPRIKSRINOIKITFKSD--DPPAASETWESVTSISGVSYNSPVT 155
DB 255 VLGPFCGSK-APEPSTOSHVLILFHSNDAENRGWRLSYRAAGNECPLOPVHGKIE 313
QY 156 ----YEV-----AKPGFIYVSLLE--DPPAASETWESVTSISGVSYNSPVT 201
DB 314 PSQAKYFFPKDQVLVSCDGVKYLKDNVEMDFQIECLKDGTMWSNKIPCKIIVDCRAPGEL 373
QY 202 DPTLIADLDDKIAEFVIEDLKYFNPSWQEDLENNYLDTPRYGRSYHDKRSKVLD 261
DB 374 EHGILTFSTRNLT--TYKSEIKY---SCQE-----PYKK----- 403
QY 262 RLNDDAKRYSCTPRNYSVN--IREELKLVNVFFPRCLLVORCG 303
DB 404 MLNNNTGTGYTCSAGQVMWNNKVLGRSL-----PTCLPV--CG 437

RESULT 20
730018
Hypothetical protein F38E9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: 730018
R:Wu, X.; Gatlung, S.
submitted to the EMBL Data Library, January 1996
A:Description: The sequence of C. elegans cosmid F38E9.
A:Reference number: 220722
A:Accession: 730018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-767 <WUX>
A:Cross-references: UNIPROT:Q20176; EMBL:U46668; PIDN:AAA93348.1; CESP:F38E9.2
C:Genetics:
A:Gene: CESP:F38E9.2
A:Introns: 13/1; 37/3; 62/1; 89/1; 127/1; 164/2; 182/1; 235/3; 269/3; 321/2; 360/1; 455/
Query Match 7.1%; Score 141.5; DB 2; Length 767;
Best Local Similarity 24.7%; Pred. No. 0.01;
Matches 77; Conservative 44; Mismatches 114; Indels 77; Gaps 19;

QY 62 GYVQSPFPNYSYPRNLLTLWRHSEENTRIQLVFNQFGLAEANDICRYD-FVEVEDIS 120
DB 232 GVHSPPKYPSEYPPPSDCWMTIHVDENSQVAIEF-VYFHLBOHKE--CIYRLILTFGIS 208
QY 121 ETS----TIINGRNGCHKEVPRIKSRINOIKITFKSDDYFAKPGFKIYVSLLEDQPPA 176
DB 289 KNSKDGKEMSEETFGGLIE-KKTIIVSKTNQISLRFSQN-SVQKTGFELRFT--KELNEC 344

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OY 177 AASE-----TWESYTSISGV-----SYNSPVTPTL 205
Db 345 AIDKNI CHHYCVTVGFKACRVGSLSSNGFSCDSTCGYLUKASNGSISPNFPEMYP 404
OY 206 IADALDKKIAEFDTVEDLLKY--FNPSWQEDLENNYL--DTPRYGRSYHDKRSKVDL 260
Db 405 NSKTCIMEI EAPDGYHI FLNFTKFNVEGMKTECAVDYVKIGDSEKLG- EYH----- 455
OY 261 DRLNDQAKRYSCTPRYVSVNIREELKLVNV---FPRCLL-VORC-GGNCC-----G 309
Db 456 ----EALLFT-TPRN--RVRIEFSSDSSVERDGFANFIADFDDECONDNAGCEHTCON 506
OY 310 TVNMRSCCNSG 321
Db 507 RLGSYVCTCNPG 518

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Search completed: November 10, 2005, 09:36:10
 Job time : 43.0683 secs

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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:21:06 ; Search time 166.998 Seconds
(without alignments)
1134.561 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 1994

Sequence: 1 MRLRLFYTLTLCANFCSCRD.....DIQLDHERDQCICSRPPR 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

1: uniprot_03:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1994	100.0	370	2	Q9GZP0
2	1949	97.7	364	2	Q9BWS5
3	1775	89.0	370	2	Q9EOT1
4	1737	87.1	370	2	Q9ZS17
5	1493	74.9	300	2	Q6V9H4
6	1141	57.2	261	2	Q8K2L3
7	753	37.8	345	2	Q91946
8	752	37.7	345	2	Q9QY71
9	750	37.6	345	2	Q8CT19
10	744	37.3	345	2	Q9E0X6
11	742.5	37.2	345	2	Q9JL22
12	742	37.2	345	2	Q9JHV8
13	741.5	37.2	345	2	Q9NRA1
14	632	31.7	258	2	Q8K429
15	189.5	9.5	707	1	BMP1_XENTLA
16	189.5	9.5	977	2	Q91325
17	188.5	9.5	735	2	Q57381
18	188.5	9.5	735	2	Q66K13
19	188.5	9.5	1007	2	Q8GJ28
20	187.5	9.4	241	2	Q9Z135
21	187.5	9.4	775	2	Q6P550
22	187.5	9.4	966	1	BMP1_HUMAN
23	187.5	9.4	991	1	BMP1_MOUSE
24	187.5	9.4	991	1	Q6N2M2
25	186.5	9.4	1015	2	Q9Y6L7
26	186.5	9.4	1078	2	Q9U000
27	184.5	9.3	3494	2	Q7LC53
28	184.5	9.3	3623	2	Q60494
29	183.5	9.2	1012	2	Q9WVW6
30	180.5	9.1	1022	1	TLD_BRARE
31	177	8.9	954	2	Q75UQ6

32	176	8.8	928	1	NRPI_XENTLA	P28824 xenopus lae
33	175.5	8.8	309	2	Q6T435	Q6T495 brachydanio
34	175.5	8.8	360	2	Q9RT53	Q9RT53 canis famli
35	175	8.8	871	2	Q6T869	Q6T869 brachydanio
36	175	8.8	959	2	Q69DB7	Q69DB7 brachydanio
37	175	8.8	959	2	Q6RT22	Q6RT22 brachydanio
38	175	8.8	959	2	Q6RT70	Q6RT70 brachydanio
39	174.5	8.8	808	2	Q7YU36	Q7YU36 drosophila
40	174.5	8.8	1019	2	Q57382	Q57382 xenopus lae
41	174.5	8.8	1067	1	TLD_DROME	P25723 drosophila
42	173.5	8.7	691	2	Q57658	Q57658 gallus gall
43	173.5	8.7	1008	2	Q9DER7	Q9DER7 gallus gall
44	173	8.7	3623	2	Q70244	Q70244 rattus norv
45	172.5	8.7	1013	2	Q43897	Q43897 homo sapien
46	172.5	8.7	1033	2	Q9N0S4	Q9N0S4 homo sapien
47	171.5	8.6	538	2	Q6AM49	Q6AM49 homo sapien
48	171.5	8.6	609	2	Q96190	Q96190 homo sapien
49	171.5	8.6	641	2	Q71SW6	Q71SW6 homo sapien
50	171.5	8.6	644	2	Q961H5	Q961H5 homo sapien
51	171.5	8.6	704	2	Q9H2E1	Q9H2E1 homo sapien
52	171.5	8.6	906	2	Q6X907	Q6X907 homo sapien
53	171.5	8.6	923	1	NRPI_HUMAN	Q14786 homo sapien
54	171.5	8.6	923	2	Q86T59	Q86T59 homo sapien
55	170.5	8.5	913	2	Q68DN3	Q68DN3 homo sapien
56	170	8.5	913	2	Q6NUE0	Q6NUE0 xenopus lae
57	169.5	8.5	746	2	Q81AD8	Q81AD8 halocynthia
58	168	8.4	914	1	NRPI_CHICK	P79795 gallus gall
59	168	8.4	923	1	Q6PAR3	Q6PAR3 mus musculu
60	167.5	8.4	3670	1	CSM014	Q72407 homo sapien
61	167	8.4	905	2	Q800L4	Q800L4 gallus gall
62	167	8.4	919	2	Q8UVR0	Q8UVR0 gallus gall
63	167	8.4	921	2	Q9OX38	Q9OX38 rattus norv
64	167	8.4	922	1	NRPI_RAT	Q8UJ99 rattus norv
65	167	8.4	936	2	Q8UJQ9	Q8UJ99 gallus gall
66	166.5	8.4	574	2	Q86RL8	Q86RL8 illyanassa o
67	166.5	8.4	923	1	NRPI_BRARE	Q8GKX6 brachydanio
68	166.5	8.4	923	2	Q69DB8	Q69DB8 brachydanio
69	166.5	8.4	1013	2	Q62381	Q62381 mus musculu
70	164.5	8.2	746	2	Q01654	Q01654 halocynthia
71	164	8.2	923	1	NRPI_MOUSE	P97333 mus musculu
72	163.5	8.2	927	2	Q6T490	Q6T490 brachydanio
73	163.5	8.2	927	2	Q6T868	Q6T868 brachydanio
74	162	8.1	579	2	Q96BD9	Q96BD9 homo sapien
75	161	8.1	579	2	Q9BY79	Q9BY79 homo sapien
76	160.5	8.0	927	2	Q69DB6	Q69DB6 brachydanio
77	159.5	8.0	677	2	Q9VYC7	Q9VYC7 drosophila
78	159	8.0	555	2	Q9H2E2	Q9H2E2 homo sapien
79	159	8.0	733	2	Q9Z0S0	Q9Z0S0 mus musculu
80	159	8.0	733	2	Q8CD27	Q8CD27 mus musculu
81	159	8.0	901	2	Q9H2D5	Q9H2D5 homo sapien
82	159	8.0	901	2	Q9H2E4	Q9H2E4 homo sapien
83	159	8.0	906	2	Q9H2D4	Q9H2D4 homo sapien
84	159	8.0	906	2	Q9H2E3	Q9H2E3 homo sapien
85	159	8.0	931	1	NRPI_HUMAN	Q60462 homo sapien
86	159	8.0	931	2	Q7Z3T9	Q7Z3T9 homo sapien
87	158	7.9	578	2	Q8BPP4	Q8BPP4 mus musculu
88	157	7.9	145	2	Q8BPP0	Q8BPP0 mus musculu
89	157	7.9	925	1	NRPI_RAT	Q35276 rattus norv
90	157	7.9	925	2	Q8QZT7	Q8QZT7 mus musculu
91	157	7.9	931	1	NRPI_MOUSE	Q53715 mus musculu
92	156.5	7.8	860	2	Q7QAH1	Q7QAH1 anopheles g
93	156.5	7.8	936	2	Q8IFX2	Q8IFX2 crassostrea
94	156.5	7.8	1524	2	Q91674	Q91674 xenopus lae
95	155	7.8	584	2	Q8K480	Q8K480 mus musculu
96	155	7.8	697	2	Q8CC43	Q8CC43 rattus norv
97	154.5	7.7	951	2	Q20176	Q20176 caenorhabdi
98	153	7.7	449	2	Q9SKA3	Q9SKA3 drosophila
99	153	7.7	701	2	Q9JUS9	Q9JUS9 rattus norv
100	153	7.7	1464	2	Q23395	Q23395 drosophila

ALIGNMENTS

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RESULT 1
O9GZPO PRELIMINARY; PRT; 370 AA.
ID O9GZPO.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Spinal cord-derived growth factor-B (MSTR036) (Placental-derived growth
DE factor D) (Iris-expressed growth factor long form).
GN Name=hSCDGF-B; Synonyms=IEGF, PDGFD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582; DOI=10.1006/brc.2000.4187;
RA Hamada T., Ue-Tel K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotenein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liaw C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2131380; PubMed=11331882; DOI=10.1038/35074593;
RA Larochelle W.J., Jeffers M., McDonald W.F., Chiklaku R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez B., Deegler L.L., Riltman B., Shinkens J.,
RA Shinkens R.A., Rothberg J.W., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11311881; DOI=10.1038/35074588;
RA Bergsten E., Uetela M., Li X., Plectras K., Ostman A., Heldin C.H.,
RA Alltalo K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wisrow G., Bernstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
RT project: steroid-response factors and similarities with retinal
RT pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
DR EMBL; AB033833; BAB18903.1; -
DR EMBL; AF133216; AAG39287.1; -
DR EMBL; AF133584; AAK38840.1; -
DR EMBL; AF136376; AAK36136.1; -
DR EMBL; AY027517; AAK20081.1; -
DR PIR; JC7591; JC7591.
DR HSSP; O9JUS8; INT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD growth factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.

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DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR PROSITE; PS0430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 370 AA; 42648 MW; D387F485E7BB7674_CNC64;
Query Match 100.0%; Score 194; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 7,7e-142;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLPYRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLPYRDETIQVKG 60
QY 61 NGVQSPRPFPNSYPNNLLTLRLHSGENTRIQLVFDNQFGEAENDICRYDFVEVDIS 120
Db 61 NGVQSPRPFPNSYPNNLLTLRLHSGENTRIQLVFDNQFGEAENDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPRIRKSRITNOIKITRSDDYFVAKGFKIYSLLEDFOPAASE 180
Db 121 ETSITIRGRWCGHKEVPRIRKSRITNOIKITRSDDYFVAKGFKIYSLLEDFOPAASE 180
QY 181 TNWESVTSISGVSNPSVTDPPTLIADALDKTIAEPTVVDLKYFNPESMOEDLEMY 240
Db 181 TNWESVTSISGVSNPSVTDPPTLIADALDKTIAEPTVVDLKYFNPESMOEDLEMY 240
QY 241 LDTPRYRGRSYHDKSKYVDLRLNDADAKRYSCTPRNTSVNIREBELKANVFFPRCLLVQ 300
Db 241 LDTPRYRGRSYHDKSKYVDLRLNDADAKRYSCTPRNTSVNIREBELKANVFFPRCLLVQ 300
QY 301 RCGNGCGGCTNNWMSCTGNSGTYKHYHEVLQEPBGHKKRGRAKTALVIOLDHHERC 360
Db 301 RCGNGCGGCTNNWMSCTGNSGTYKHYHEVLQEPBGHKKRGRAKTALVIOLDHHERC 360
QY 361 DCICSSRPFR 370
Db 361 DCICSSRPFR 370
RESULT 2
O9BWVS PRELIMINARY; PRT; 364 AA.
ID O9BWVS.
AC O9BWVS.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Iris-expressed growth factor short form (Platelet derived growth
DE factor D, isoform 2) (SCDGF-B).
GN Name=IEGF; Synonyms=PDGFD; ORFNames=UNQ1899;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RX MEDLINE=22103462; PubMed=12107412;
RA Wisrow G., Bernstein S.L., Ray S., Wyatt M.K., Behal A., Touchman J.W.,
RA Bouffard G., Smith D., Peterson K.;
RT "Expressed sequence tag analysis of adult human iris for the NEIBank
RT project: steroid-response factors and similarities with retinal
RT pigment epithelium.";
RL Mol. Vision 8:185-195(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscdin T.B., Toshimiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Mañan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RA Strausberg R.;
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RP (4)
RX SEQUENCE FROM N.A.
RA MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gunney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seabright S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RT Genome Res. 13:2265-2270(2003).
DR EMBL; AY027518; AAK20082.1; -.
DR EMBL; BC030645; AAH30645.1; -.
DR EMBL; AY359116; AAO89474.1; -.
DR PIR; JCT591; JCT591.
DR HSSP; Q9JUS8; LNT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDDEA9EAC_CRC64;

Query Match 97.7%; Score 1949; DB 2; Length 364;
Best Local Similarity 98.4%; Pred. No. 1.8e-138;
Matches 364; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 MHRLLIVYLLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRRETIQVKG 60
DB 1 MHRLLIVYLLICANFSCCRDTSATPOSASIKALRNANLRD-----DLRRRETIQVKG 54

QY 61 NGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
DB 55 NGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 114

QY 121 ETSITIRGRWCGHKEVPRIKSRITQIKITPKSDDYFVAKPGFKIYYSLEDFQPAASE 180
DB 115 ETSITIRGRWCGHKEVPRIKSRITQIKITPKSDDYFVAKPGFKIYYSLEDFQPAASE 174

QY 181 TNNESTVTSISGVSYSVPSVTPDPTLADALDKKIAEDTVEDLLKYNPESWODELENNY 240
DB 175 TNNESTVTSISGVSYSVPSVTPDPTLADALDKKIAEDTVEDLLKYNPESWODELENNY 234

QY 241 LDPTRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLLYQ 300
DB 241 LDPTRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLLYQ 300

DB 235 LDPTRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLLYQ 294
QY 301 RCGGNGCGTVMWRSCCTGSKTKVKKYHEVLOPEPHIKRGRAKTMALVDIOLDHHERC 360
DB 295 RCGGNGCGTVMWRSCCTGSKTKVKKYHEVLOPEPHIKRGRAKTMALVDIOLDHHERC 354

QY 361 DCICSSRPPR 370
DB 355 DCICSSRPPR 364

RESULT 3
Q9E0T1 PRELIMINARY; PRT; 370 AA.
ID 09E0T1;
AC 09E0T1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN Name=SCDGF-B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21092670; PubMed=11162582; DOI=10.1006/dbrc.2000.4187;
RA Hamada T., Ue-Tel K., Imaki U., Miyata Y.;
RT "Molecular cloning of SCDGF-B, a novel growth factor homologous to
RT SCDGF/PDGF-C/fallotectin.";
RT Biochem. Biophys. Res. Commun. 280:733-737(2001).
DR EMBL; AB052170; BAB18920.1; -.
DR PIR; JCT592; JCT592.
DR HSSP; Q9UCV4; INZ1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73_CRC64;

Query Match 89.0%; Score 1775; DB 2; Length 370;
Best Local Similarity 86.8%; Pred. No. 2.3e-125;
Matches 321; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 MHRLLIVYLLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRRETIQVKG 60
DB 1 MHRLLIVYLLICANFSCCRDTSATPOSASIKALRNANLRD-----DLRRRETIQVKG 54

QY 61 NGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
DB 61 TGVQSPRPFPNSYPRNLLTWRLHSGENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120

QY 121 ETSITIRGRWCGHKEVPRIKSRITQIKITPKSDDYFVAKPGFKIYYSLEDFQPAASE 180
DB 121 ETSITVIRGRWCGHKEVPRIKSRITQIKITPKSDDYFVAKPGFKIYYSLEDFQPAASE 180

QY 181 TNNESTVTSISGVSYSVPSVTPDPTLADALDKKIAEDTVEDLLKYNPESWODELENNY 240
DB 181 TNNESTVTSISGVSYSVPSVTPDPTLADALDKKIAEDTVEDLLKYNPESWODELENNY 240

QY 241 LDPTRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLLYQ 300
DB 241 MOTPRYRGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIIBELKLANVFFPRCLLYQ 300

QY 301 RCGGNGCGTVMWRSCCTGSKTKVKKYHEVLOPEPHIKRGRAKTMALVDIOLDHHERC 360
DB 301 RCGGNGCGTVMWRSCCTGSKTKVKKYHEVLOPEPHIKRGRAKTMALVDIOLDHHERC 360

OY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 4
ID 092517 PRELIMINARY; PRT; 370 AA.
AC 092517; Q9P1L8; 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, last annotation update)
DE placental-derived growth factor D (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109
DE product:placental-derived growth factor D).
DE Name:Pgfd.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c;
RX MEDLINE=21231380; PubMed=11331882; DOI=10.1038/35074593;
RA Larochele W.J., Jeffers M., McDonald W.F., Chiklaku R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boidog F.L., Yang M., Vernet C.,
RA Bugese C.E., Fernandez E., Deegler L.L., Rittman B., Shinkens J.,
RA Shinkens R.A., Rochberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Proteinase-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20499774; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kuthara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Soabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335583; AAK38839.1; -
DR EMBL; AK003359; BAB22735.2; -
DR HSSP; Q9J3S8; 1NTO.
DR MGD; MG1:1919035; Pgfd.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IDA.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SMO0141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
SQ SEQUENCE 370 AA; 42809 MW; 988084CF6813BFBF CRC64;

Query Match 87.1%; Score 1737; DB 2; Length 370;
Best Local Similarity 85.1%; Pred. No. 1.7e-122;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

OY 1 MRLIFVYTLICANFCSCRDTSATPQASIALRNALRDESNHLLDLYRDETYQKG 60
Db 1 MRLVLSILLCANFSCYDPFATPQASIALRNALRDESNHLLDLYRDEENIQVTS 60
OY 61 NGVOSPEFNSYPRNLLTLRLHSEQENTRIOLVFNDFGLBEANDICRYDFVEEIS 120
Db 61 NGHVOSPEFNSYPRNLLTLRLHSEQENTRIOLVFNDFGLBEANDICRYDFVEEIS 120
OY 121 ETSITIRGMCHEKPEPRISRTNQTITKESDYPFAKKGFKIYSLLEDFCPAAASE 180
Db 121 EESTYVRMRMGHKEIPRISRTNQTITKESDYPFAKKGFKIYSFVEDFOEAASE 180
OY 181 TNWESVTSSISGVSYNSPVTPTLADALDKIAEFTVEDLKYFNPESQEDLENNY 240
Db 181 TNWESVTSSISGVSYNSPVTPTLADALDKIAEFTVEDLKYFNPESQEDLENNY 240
OY 241 LDTPRYGRSYHDKRSKVDLRLNDADKRYSCPTPNYSVNTREELKLANVFFPCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLRLNDADKRYSCPTPNYSVNTREELKLANVFFPCLLVQ 300
OY 301 RCGNCGCGTNNWRSCTGNSGTVKKAHEVLOFEBGHIKRRGRAKTMAVLDIOLDHFRRC 360
Db 301 RCGNCGCGTNNWRSCTGNSGTVKKAHEVLOFEBGHIKRRGRAKTMAVLDIOLDHFRRC 360
OY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 5
ID 06V9H4 PRELIMINARY; PRT; 300 AA.
AC 06V9H4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, last annotation update)
DE It's-expressed growth factor (fragment).
GN Name=PDGFD;

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OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RA Ray S., Mielow G.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347260; AAQ24382.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 1
FT TER 300
SQ SEQUENCE 300 AA; 34616 MW; 716C873C9C01C0C6 CRC64;

Query Match 74.9%; Score 1493; DB 2; Length 300;
Best Local Similarity 91.3%; Pred. No. 3e-104;
Matches 274; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 57 QVNGNGYVSPRPNSYPRNLLTWRLHSGENTRIQVFNQGLBEAENDICRYDVEV 116
DB 1 QVNGNGYVSPRPNSYPRNLLTWRLHSGENTRIQVFNQGLBEAENDICRYDVEV 60
QY 117 EDISSTIIRGMCQKHEVPRRIKSTNOIKITFKSDDYFVAKPGFKIYSLLEDFQPA 176
DB 61 EDISSTIIRGMCQKHEVPRRIKSTNOIKITFKSDDYFVAKPGFKIYSLLEDFQPA 120
QY 177 AASETWESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKYNESQOEDL 236
DB 121 AASETWESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKYNESQOEDL 180
QY 237 ENNYLTPRYGRSYHDKRSKVDLRLNDPAKRYSCPRYSVNIKEELKLVAVVPPRC 296
DB 181 ENNYLTPRYGRSYHDKRSKVDLRLNDPAKRYSCPRYSVNIKEELKLVAVVPPRC 240
QY 297 LTVQRCGNGCGCTVWNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTALVDIQLDH 356
DB 241 LTVQRCGNGCGCTVWNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGAKTALVDIQLDH 300

RESULT 6
O8K2L3
ID O8K2L3; PRELIMINARY; PRT; 261 AA.
AC O8K2L3;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Pdgd protein.
GN Name=PDGf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RL MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleorn M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Uebin T.B., Toshlyuki S., Caramini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RL Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030896; AAH30896.1; -.
DR HSSP; Q9JUS8; INT0.
DR MGD; MGI:1919035; Pdgd.
DR GO; GO:0005615; C:extracellular space; TMS.
DR GO; GO:0050730; P:regulation of peptidyl-L-tyrosine phosphoryla. . . ; IDA.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 261 AA; 30228 MW; 2EEC3F637A52D09 CRC64;

Query Match 57.2%; Score 1141; DB 2; Length 261;
Best Local Similarity 82.5%; Pred. No. 7.8e-78;
Matches 212; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

QY 1 MHRLLFVYLLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRRBETIOVGK 60
DB 1 MHRLLFVYLLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRRBETIOVGK 60
QY 121 ERTITIRGMCQKHEVPRRIKSTNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
DB 121 ERTITIRGMCQKHEVPRRIKSTNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
QY 121 ERTITIRGMCQKHEVPRRIKSTNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
DB 121 ERTITIRGMCQKHEVPRRIKSTNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
QY 181 TWESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKYNESQOEDL 240
DB 181 TWESYTSISGVSYNSPSVTDPTLTADALDKKIAEFDTVEDLLKYNESQOEDL 240
QY 241 LDPTRYGRSYHDKRSK 257
DB 241 LDPTRYGRSYHDKRSK 257

RESULT 7
Q91946
ID Q91946; PRELIMINARY; PRT; 345 AA.
AC Q91946;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Spinal cord-derived growth factor.
GN Name=SCDGF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=white leghorn; TISSUE=spinal cord;
RL MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ue-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";

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RL EBS Letc. 475:97-102(2000).
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC EMBL; AB033829; BAB03265.1; -.
DR HSSP; O9J58; INT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR Growth factor; Mitogen.
KW SEQUENCE 345 AA; 38940 MW; 97ACEA92B5128C CRC64;
SQ
Query Match 37.8%; Score 753; DB 2; Length 345;
Best Local Similarity 46.6%; Pred. No. 1.8e-48;
Matches 153; Conservative 54; Mismatches 91; Indels 30; Gaps 9;
QY 42 ESNHLLDLYRDETTQVKGNGVQSPFPNSYPRNLLTLWRHS-OENTRIQLVFDNQG 100
DB 37 EONGVOD-FQHEKITLVTSNGSIHSPKPHYPRNTVLVRLVAADENWIDLTEDERG 95
QY 101 LEEAENDICRYDFVEVEDISESTIRGRCGKHKEVPRPKRTNOIKTFESDDYFVK 160
DB 96 LDDPEDDICKYDFVEVEEPPSDGTVL--GRWCGSSSVSPFSQISKGNQIRIRFVSDTFPSQ 153
QY 161 PCFKIYSLHEDFOPAAASETSMESVTSISGVSNVSPSTPPT-LIADALDKLIAEPT 219
DB 154 PCFCIHVTLVLVHHTEAP-----SPSSLPSPSLPLDVLNNAVAGFT 195
QY 220 VEDDLKYPFESVQEDLEMYITDTPRYGRSY-HDRKSK-VLLDRINDAKYSCTPPNY 277
DB 196 VELRLRYLEPDRWQDLLEDLYRPTQLGKAYIHGRKSRVVDLNLKEVRLYSCTPRNF 255
QY 278 SVNIREELKLVAVFPFRCLLVORCGGCGGTVMWRSTCNCSGKTVKHYHVLQEPBH 337
DB 256 SVSLBELKRTDTTTPWPLCLLVKRCGAGNACCHQNCNCCQCPRTVKYKXHEVLQKP-- 313
QY 338 IKRRG-RAKTVALVDIQLDHHRCDCIC 364
DB 314 --RSGVRGLHKSLTVPLEHHECCVC 339

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RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/Gr.145100;
RA Carinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komio H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/Gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carinci P.,
RA Komio H., Akiyama J., Nishi K., Katsuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Otsawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carinci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Keigawa I., Katsukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komio H., Koda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF117608; AAF22516.1; -.
DR EMBL; AF266467; AAK58566.1; -.
DR EMBL; AK033734; BAC28455.1; -.
DR EMBL; AK042767; BAC31358.1; -.

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DE Spinal cord-derived growth factor.
GN Name=rsdcgf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar; TISSUE=Kidney;
RX MEDLINE=21092670; PubMed=1162582; DOI=10.1006/bhrc.2000.4187;
RA Hamada T., Ui-Tel K., Imaki J., Miyata Y.;
RT "Molecular cloning of SCDF-B, a novel growth factor homologous to
RT SCDF/PDGF-C/fallotectin.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL: AB031830; BAB1969.1; -.
DR HSPF; Q9JUS8; INT0.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR Growth Factor; Mitogen.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6EB9765D10 CRC64;

Query Match 37.3%; Score 744; DB 2; Length 345;
Best Local Similarity 45.3%; Pred. No. 8.6e-48;
Matches 148; Conservative 60; Mismatches 91; Indels 28; Gaps 10;

QY 42 ESNHLTDLVRRDETIOVKGNGVYSPRPNSYRNLLTWRLHS-QENTRIQLVFDNQFG 100
DB 37 EQNGVQD-PRHBRVVTISGNSIHSPKPHYPRRTVLVWRLVAVDENVRIQLTFDERG 95
QY 101 LEEAENDICRDYFVEVEDISSTIIRGWCCHKVEYPPRIKRTNQIKTFPSDDYPAK 160
DB 96 LEDPDDDLCKXDFVEVEEPPSDSV--GRWCSGGVTPGKQTSKGNHIRRFVSDYFPSE 153
QY 161 PGFKLYSLTLEDFOPAAASETNWESVTSISGVSNSPGCTVPTLLA-DALDKTAAEPDT 219
DB 154 PGFCIHYSI---MQVETTT-----SSVLPSPALSIDLNNAVTANST 195
QY 220 VEDLLKYFNESQEDLENMVLDPFRYGRSY-HDRKSK-VDLRLNDAKRYSCTPRNY 277
DB 196 VEELIRFLEPPDRWQIDLSLKYPTWPLLGKAFLYGKSKXAVNLNLKEVKLYSCTPRNF 255
QY 278 SVNITEELKLANVFFPRCLLVQRCGNGCGCTVWNRSTGNSGTVYKKYHVLQPEEGH 337
DB 256 SVSIEEELKRDVTITFWPGCLLVKRCGNCACCLHNCNEQCVPRVTKYKHEVLQLRP-K 314
QY 338 IKRGRAKTMALVDIQLDHERCDIC 364
DB 315 IGKGLHK--SLTDVALEHHECDVC 339

RESULT 11
Q9UL22
ID Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TRENBLREL 13, Created)
DT 01-MAY-2000 (TRENBLREL 13, Last sequence update)
DT 05-JUL-2004 (TRENBLREL 27, Last annotation update)
DE Secretary growth factor-like protein fallotectin (Spinal cord-derived
DE growth factor) (platelet-derived growth factor C) (VEGF-E).
GN Name=hbcdgf; Synonyms=PDGFC; ORFNames=UN0174;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=20461776; PubMed=11004490; DOI=10.1016/S0167-4781(00)00066-X;
RA Tsai Y.J., Lee R.K., Lin S.P., Chon Y.H.;
RT "Identification of a novel platelet-derived growth factor-like gene,
RT fallotectin, in the human reproductive tract.";
RL Biochim. Biophys. Acta 1492:196-202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496; DOI=10.1016/S0014-5793(00)01640-9;
RA Hamada T., Ui-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552; DOI=10.1074/jbc.M101056200;
RA Gliberson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.B., Hart C.E.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RT binds to PDGF alpha and beta receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Devel B., Dowd P.,
RA Bacon D., Foster J., Grimaldi C., Gu Q., Hoss P.E., Helms S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshaigiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.
DR EMBL; AF260738; AAK51637.1; -.
DR EMBL; AY358493; AAO88857.1; -.
DR HSPF; Q9JUS8; INT0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 37.2%; Score 742.5; DB 2; Length 345;
Best Local Similarity 43.6%; Pred. No. 1.1e-47;
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVTLICANFCSDRDSATPQSAISYALRNANLRDSENHLTLVRRDETIOVKGNGV 64
DB 3 LFGLLITSALAGQGGQGAENSLSSKRFQSN--KQNGVQD-PQERRITVSTNGSI 58
QY 65 QSPFPNSYRNLLTWRLHS-QENTRIQLVFDNQFGEAENDICRDYFVEVEDISSETS 123
DB 59 HSPRPHTYPRNTLVWRLVAVDENVRIQLTFDERFGLEDEDEDICXDFVEVEEPPSDGT 118
QY 124 TIRGRGCHKEVPPRIKRTNQIKTFPSDDYPAKGFYKYSL-LEDQPAASAETN 182

Db 119 --ILGRWCGSGTVPKGQISKGNQIRIRFVSDXEPSEPGCHINYIMVQFTEAV----- 171
 QY 183 MESVTSISIGSVSNSSVTDPT-LIADALDKIAEFDYEDLLKYTNPESWQEDLENMVL 241
 Db 172 -----SSSVLPSPALPDLNLNNAITASTLEDLLRYLEPERWQDLDELYR 217
 QY 242 DTPRYGRASY-HDRKSK-VLDRLNDADKAKRSCTPNYSVNIIEELKLANVFFPRCLY 239
 Db 218 PTWQLLGKAFVPRKSRKRVLDNLITEEVRLYSCTPNPFVSIEELKRTDTITWPGCLY 217
 QY 300 QRCGNGCGGTVMNRSCTCNSGKTVKKYHEVLOFEPGHTKRRAKTMALVDIOLDHNER 359
 Db 278 KRCGNGCACCLHNCNCCQCPVSKYTKKYHEVLQLRP---KTGVRGLHKSLTDVALBHEHE 314
 QY 360 CDCIC 364
 Db 335 CDCVC 339

RESULT 12

Q9JHV8 PRELIMINARY; PRT; 345 AA.
 AC Q9JHV8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Platelet-derived growth factor C.
 GN Name=PDGFC;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10050;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss-Webster/NIH;
 RA MEDLINE=20417814; PubMed=10960785; DOI=10.1016/S0925-4773(00)00425-1;
 RX Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
 RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
 organogenesis";
 RL Mech. Dev. 96:209-213(2000).
 DR EMBL; AF286725; AAF91483.1; -.
 DR HSSP; Q9JVS8; INTO.
 DR MGD; MGI:1859631; PDGFC.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005461; F:platelet-derived growth factor receptor bin.; IDA.
 DR GO; GO:0008284; P:regulation of cell proliferation; IDA.
 DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla.; IDA.
 DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin.; IDA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS00180; CUB; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 SO SEQUENCE 345 AA; 38866 MW; FA1486BED6D362F8 CRC64;

Query Match 37.2%; Score 742; DB 2; Length 345;
 Best Local Similarity 45.0%; Pred. No. 1.2e-47;
 Matches 147; Conservative 59; Mismatches 93; Indels 28; Gaps 9;

QY 42 ESNRLDLYRDETIOVKGNGVQSPRPNSYPRNLLTWRLHS-QENTRIQLVFNQNG 100
 Db 37 EQGVQVD-PRHEVVTISGNGSIHSPFHTYPRNVLWRLVAVDNVTQLTDFERFG 95
 QY 101 LEEAENDICRYDEVEVEDISSETIIRGRWCGHKEVPRIKSRNQIKITFKSDDYFAK 160
 Db 96 LEEPDDEICKYDVEVEEPPSDSVL--GRWCGSETVPGKQTSKGNHRIKRVFVDEYFPSE 153
 QY 161 PGKRIYSLLEDQOPAAASTNWSVTSISGVSNSSVTDPT-LIADALDKIAEFDY 219
 Db 154 PGFCIHYSIT--MPQVTEIT-----SSSVLPSPSLDNLNNAITASTLEDLLRYLEPERWQDLDELYR 195

QY 220 VEDLTKEFNPESWQEDLENMVLDTTPRYGRASY-HDRKSK-VLDRLNDADKAKRSCTPRNY 277
 Db 196 LEEELIYLPDPKQVQDLDBLYKPTWQLLGKAFYVKKSKYVNLNLKEEVLKYSTPRNF 255
 QY 278 SVNIIEELKLANVFFPRCLLYQRCGNGCGGTVMNRSCTCNSGKTVKKYHEVLOFEPGH 317
 Db 256 SVSIREELKRTDTRFMPGCLLYVRGCGNACCLHNCNCCQCPVSKYTKKYHEVLQLRP-- 313
 QY 338 IKRRGAKTMALVDIOLDHNERCDCIC 364
 Db 314 -KTGVKGLHKSLTDVALBHEHECDCVC 339

RESULT 13

Q9NRAL PRELIMINARY; PRT; 345 AA.
 AC Q9NRAL;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Platelet-derived growth factor C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=20268201; PubMed=10806482; DOI=10.1038/35010579;
 RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uutela M.,
 RA Backstrom G., Helstrom M., Boström H., Li H., Soriano P.,
 RA Betscholtz C., Heldin C.-H., Allitalo K., Ostman A., Eriksson U.;
 RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
 receptor";
 RL Nat. Cell Biol. 2:302-309(2000).
 RC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
 DR EMBL; AF244813; AAF80597.1; -.
 DR HSSP; Q9JVS8; INTO.
 DR GeneW; HGNC:8801; PDGRC.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0008283; P:cell proliferation; IEA.
 DR GO; GO:0000074; P:regulation of cell cycle; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000072; PD_growth_factor.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS00180; CUB; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 DR Growth factor; Mitogen.
 SO SEQUENCE 345 AA; 39043 MW; 590889CEA55C5EA CRC64;

Query Match 37.2%; Score 741.5; DB 2; Length 345;
 Best Local Similarity 43.6%; Pred. No. 1.3e-47;
 Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 5 IFVYLLICANFSCSRDTSATPOSASIKALRMANLRDESNHLLTDLRYRDETIOVKGNGV 64
 Db 3 LFEILLVTSLALAGRGTOAESNLSSKQFSSN---KEGVQVD-PQHEIITVSTGSI 58
 QY 65 QSPRPNSYPRNLLTWRLHS-QENTRIQLVFNQNGLEAENDICRYDVEVEEDISSETS 123
 Db 59 HSPRPHTYPRNVLWRLVAEENWIDLTDFERGLEDPEDDICKYDVEVEEESDGT 118
 QY 124 TIRGRWCGHKEVPRIKSRNQIKITFKSDDYFAKPGFKIYYS-LDFOPAAASET 182
 Db 119 --ILGRWCGSGTVPKGQISKGNQIRIRFVSDXEPSEPGCHINYIMVQFTEAV----- 171
 QY 183 MESVTSISIGSVSNSSVTDPT-LIADALDKIAEFDYEDLLKYTNPESWQEDLENMVL 241
 Db 172 -----SSSVLPSPALPDLNLNNAITASTLEDLLRYLEPERWQDLDELYR 217

Oy		242	DTPRKRGSSY-HDRSK-VDDLRLNDADKARYGCTPRNYSVNIREEKLKANVFPPRCLLV	299
Db		218	PTWQLGLGAFFGGRSRVVLDLTLTEEVRLYSTCPNFVSIREELIKRDTITFWPDCLLV	277
Oy		300	ORCGNGCCGGTVNWRSGTCSGKTAKKYVEVLQFEFGHKKRGRKATMALVIQLDHHBR	359
Db		278	KRCGNCACCLHNCGECQVPSPKVTKKHVEVLQLR---KTGVRLGHSLTJVALEHBE	334
Oy		360	CDCIC 364	
Db		335	CDCVC 339	
 RESULT 14				
ID	QBK429		PRELIMINARY; PRT;	258 AA.
AC	QBK429;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Placetal-derived growth factor C (fragment).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Skin;			
RA	Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;			
RL	Submitted (May-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF508348; AAM47265.1; --			
DR	HSSP: Q9JJS8; INTO.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0008083; F:growth factor activity; IEA.			
DR	GO; GO:0008151; P:cell growth and/or maintenance; IEA.			
DR	InterPro; IPR000859; CUB.			
DR	InterPro; IPR000072; PD_growth_factor.			
DR	Pfam; PF00431; CUB; 1.			
DR	SMART; SM00042; CUB; 1.			
DR	PROSITE; PS01180; CUB; 1.			
DR	PROSITE; PS0278; PDGF_2; 1.			
FT	NON TER	1		
FT	NON TER	1		
SQ	SEQUENCE	258 AA; 29255 MW; 88625B989FC3F8B CRC64;		
 Query Match 31.7%; Score 632; DB 2; Length 258; Best Local Similarity 44.9%; Pred. No. 1.6e-39; Matches 122; Conservative 54; Mismatches 72; Indels 24; Gaps 7				
Oy		51	RRDETIOVKNGNVOSPSPRPNSYPNNLLLTWLHS-QENTRIOLVPDNQGLEAEANDIC	109
Db		4	RHERVVTISGNGSINSPKPHTYPNRYLVWRLVADEVNRILQLTDERFGLDPDDLC	63
Oy		110	RYDFEVEDISETSTIIIGRWGCKHEVPRIRKSRTNOIKITEPKSDDYFVAKGFKIYSL	169
Db		64	KYDFEVEBPSPGSLV--GRWGSGSTVPEKQSKSNHRIIRVDSDEYPSSEGFCHISI	121
Oy		170	LEDFOPAALASETNWESVTSISGVSYNPSVTDPLIA-DALDKIAEDTVLEDLIKFPN	228
Db		122	I---MPQVTEFT-----SPSVLPSPSALSIDLLNNAVTAFSTIEBELIRPLE	163
Oy		229	PESWOEDLENMYLDTPRYRGREY-HDRSK-VDLRLINDADKARYGCTPRNYSVNIREEKL	286
Db		164	PDRWDIDDSLXYKPWPPLLGKAFVLGKSKSAVNLDKEVKLYSCTPRNFSVSIREEKL	223
Oy		287	LANVVFPPRCCLIVORCGNGCGGTWNBSCTC 318	
Db		224	RTDTIFWPDCLLVKRGGCACCLHNCNCCQ 255	
 RESULT 15				
MPI_XENLA				

ID	BMP1_XENLA	STANDARD;	PRT:	707 AA.
AC	P96070;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DS	Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_Taxid=83355;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RC	MEDLINE=94065787; PubMed=8262384; DOI=10.1016/0378-1119(93)90103-A;			
RA	Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;			
RT	"Cloning and expression of cDNA encoding Xenopus laevis bone			
RT	morphogenetic protein-1 during early embryonic development.";			
RL	Gene 134:257-261(1993).			
CC	-1- FUNCTION: Involved in pattern formation in gastrula and later			
CC	differentiation of developing organs.			
CC	-1- DEVELOPMENTAL STAGE: Blastula, early gastrula and hatched			
CC	tadpoles. Little or no expression in morula and late gastrula.			
CC	-1- SIMILARITY: Belongs to the peptidase M12A family.			
CC	-1- SIMILARITY: Contains 1 EGF-like domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J12249; AAA16313.1; -.			
DR	PIR; JC2218; JC2218.			
DR	HSSP; P01130; 1H28.			
DR	MEROPS; M12.005; -.			
DR	InterPro; IPR000152; Asx_hydroxyl_S.			
DR	InterPro; IPR000859; CUB_2.			
DR	InterPro; IPR000742; EGF_2.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR006209; EGF_Like.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	InterPro; IPR001506; Peptidase_M12A.			
DR	Pfam; PF01400; Astacin; 1.			
DR	Pfam; PF00431; CUB; 3.			
DR	Pfam; PF00068; EGF; 1.			
DR	PRINTS; PR00480; ASTACIN.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.			
DR	PROSITE; PS01180; CUB; 3.			
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.			
DR	PROSITE; PS01866; EGF_2; 1.			
DR	PROSITE; PS00262; EGF_3; 1.			
DR	PROSITE; PS00187; EGF_CA; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			
KW	Calcium; Chondrogenesis; Cytokine; EGF-like domain; Growth factor;			
KW	Hydrolase; Metalloprotease; Osteogenesis; Protease; Repeat; Signal;			
KW	Zinc.			
FT	SIGNAL	1	?	Potential.
FT	PROPEP	?	83	Potential.
FT	CHAIN	84	707	Bone morphogenetic protein 1.
FT	DOMAIN	84	284	Metalloprotease.
FT	DOMAIN	285	397	CUB 1.
FT	DOMAIN	398	509	CUB 2.
FT	DOMAIN	510	551	EGF-like, calcium-binding (Potential).
FT	DOMAIN	554	666	CUB 3.
FT	METAL	176	176	Zinc (catalytic) (By similarity).
FT	ACT_SITE	177	177	By similarity.
FT	METAL	180	180	Zinc (catalytic) (By similarity).
FT	METAL	186	186	Zinc (catalytic) (By similarity).
FT	DISULFID	146	149	By similarity.

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FT DISULFID 514 526 By similarity.
FT DISULFID 522 535 By similarity.
FT DISULFID 537 550 By similarity.
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 105 105 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 326 326 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 562 562 N-linked (GlcNAc...) (Potential)
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC9B8D CRC64;

Query Match
Best Local Similarity 42.5%; Score 189.5; DB 1; Length 707;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

QY 59 KNGGYVQSPFPNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVD 118
DB 560 KUNGSTNSGWPKEYPNNKCIWQVAPYRISLKFQ-QF--ETEGNDVCKYDFVEVRS 616
QY 119 ISETSTIIRGRCWGHKEVPPRIKSRNQIKITFKSDYFVAKGPFK 164
DB 617 GLTSDSKLHGKFCG-SELPAVITSOYNNMRIFKSDN-TVSKKGPFQ 660

RESULT 16
ID Q91925 PRELIMINARY; PRT; 977 AA.
AC Q91925;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE xtd protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Lin J., Maeda R., Ong R., Kim J., Kung H., Maeno M.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83476; BA011922.1; -.
DR HSSP; P01130; 1H28.
DR GO; GO:0008533; F-actin activity; IEA.
DR GO; GO:0005509; F-actin monomer binding; IEA.
DR GO; GO:0008237; F-actin monomer binding; IEA.
DR GO; GO:0005508; P-protein synthesis; IEA.
DR Pfam; PF01400; Ascln; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PRO0480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZMGC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS0026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 977 AA; 110199 MW; 4D7D2E37C64FDF1F CRC64;

Query Match
Best Local Similarity 42.5%; Score 189.5; DB 2; Length 977;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

QY 59 KNGGYVQSPFPNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVD 118
DB 588 KUNGSTNSGWPKEYPNNKCIWQVAPYRISLKFQ-QF--ETEGNDVCKYDFVEVRS 644
QY 119 ISETSTIIRGRCWGHKEVPPRIKSRNQIKITFKSDYFVAKGPFK 164
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DB 645 GLTSDSKLHGKFCG-SELPAVITSOYNNMRIFKSDN-TVSKKGPFQ 668

RESULT 17
ID O57381 PRELIMINARY; PRT; 735 AA.
AC O57381;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein 1b.
GN Name=BMP-1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RA Goodman S., Albano R., Matthews G., Tannahill D., Dale L.;
RT "BMP-1 related proteins promote the development of ventral mesoderm in
RT early Xenopus embryos."
RL Dev. Biol. 194;144-157(1998).
DR HSSP; P01130; 1H28.
DR HSSP; Y09660; CAA70853.1; -.
DR GO; GO:0008533; F-actin activity; IEA.
DR GO; GO:0005509; F-actin monomer binding; IEA.
DR GO; GO:0008237; F-actin monomer binding; IEA.
DR GO; GO:0005508; P-protein synthesis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001506; Peptidase M12A.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01400; Ascln; 1.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PRO0480; ASTACIN.
DR SMART; SM00042; CUB; 3.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS0026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 735 AA; 83575 MW; 45B29C813F79DBE2 CRC64;

Query Match
Best Local Similarity 42.5%; Score 188.5; DB 2; Length 735;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

QY 59 KNGGYVQSPFPNSYPRNLLLTWRHLSQENTRIQLVFNQFGLAEANDICRYDFVEVD 118
DB 587 KUNGSTNSGWPKEYPNNKCIWQVAPYRISLKFQ-QF--ETEGNDVCKYDFVEVRS 643
QY 119 ISETSTIIRGRCWGHKEVPPRIKSRNQIKITFKSDYFVAKGPFK 164
DB 644 GLTSDSKLHGKFCG-SELPAVITSOYNNMRIFKSDN-TVSKKGPFQ 687

RESULT 18
ID Q66K13 PRELIMINARY; PRT; 735 AA.
AC Q66K13;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
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DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
DE BMP-1 protein.
GN Name=BMP-1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachler M., Soares M.B., Bonaldo M.F., Casavate T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gernard D.S.,
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080382; AAH80382.1; -.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 3.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 735 AA; 83603 MW; 3D24DF66AFAEBE4 CRC64;

Query Match 9.5%; Score 188.5; DB 2; Length 735;

Best Local Similarity 42.5%; Pred. No. 1.5e-05;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;
QY 59 KGVGVSPRPSPNSYPRNLLTLWRHSGOENTRIQVLPDNOGCLAEVNDICRYFVEVD 118
DB 587 KLVNSITSPGPKYPPKNCVWQVAPTOYRISLKPQ-QF--ETEGADVCKYDFEVR 643
QY 119 ISETSTIRGRGCHKEVPRPKSRITQIKITFKSDVDFVAKPGPK 164
DB 644 GLTDSKLGKFCG-TSLPAVITSOYNNMRLEFKSDN-TVSKKGRQ 687
RESULT 19
ID 08J128 PRELIMINARY; PRT; 1007 AA.
AC 08J128;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE Xoloid-like metalloprotease.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22352451; PubMed=12464431; DOI=10.1016/S0925-4773(02)00359-3;
RA Dale L., Evans W., Goodman S.A.,
RT "Xoloid-related: A novel BMP1/Toll-like-related metalloprotease
RT expressed during early Xenopus development.";
RL Mech. Dev. 119:177-190 (2002).
DR EMBL; AF393242; AAM73675.1; -.
DR HSR; P00736; IABQ.
DR MEROPS; M12.016; -.
DR GO; GO:0008533; F:actin activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008237; F:metalloprotease activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR EGF-like domain; Metalloprotease; Protease.
SQ SEQUENCE 1007 AA; 114364 MW; 3F3C686A7BF230C CRC64;
Query Match 9.5%; Score 188.5; DB 2; Length 1007;
Best Local Similarity 22.3%; Pred. No. 2.2e-05;
Matches 81; Conservative 44; Mismatches 118; Indels 121; Gaps 16;
QY 13 ANFCSCRTSATPGAS-----IKALRNANLRDESNHLLTDLVRRDET-----IQVKNQY 63
DB 564 ANFLKEDEECARPDGCGEGRCVNTLGSYKSCSDGTYLAPDKKSCFAAGGLTLKNGT 623
QY 64 VQSPRPNSYPRNLLTLWRHSGOENTRIQVLPDNOGCLAEVNDICRYDFVEVDISETS 123

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:31:47 : Search time 165 Seconds
(without alignments)
867.281 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 370

Sequence: 1 MHRILFVYLICANFCSCRD.....DIQLDHERCDICSSRPPR 370

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 5

Total number of hits satisfying chosen parameters: 74988

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	370	3	AA996864
2	370	100.0	370	3	AA848653
3	370	100.0	370	3	AA771130
4	370	100.0	370	4	AA660888
5	370	100.0	370	4	AAU00704
6	370	100.0	370	4	AAU00698
7	370	100.0	370	4	AA656601
8	370	100.0	370	4	AAE00999
9	370	100.0	370	4	AA855529
10	370	100.0	370	5	AAE15819
11	370	100.0	370	5	AA879643
12	370	100.0	370	5	AA892893
13	370	100.0	370	5	AA847891
14	370	100.0	370	5	AA879588
15	370	100.0	370	5	ABG78502
16	370	100.0	370	5	ABG76575
17	370	100.0	370	5	ABG64733
18	370	100.0	370	5	ABP51640
19	370	100.0	370	6	ABU72430
20	370	100.0	370	6	ABG76397
21	370	100.0	370	6	ABR80134
22	370	100.0	370	6	ABR43944
23	370	100.0	370	7	AAE38476
24	370	100.0	370	7	ABW02697
25	370	100.0	370	7	ADG47746

26	370	100.0	370	8	ADJ32755
27	370	100.0	370	8	ADL78000
28	370	100.0	370	8	ADL67182
29	370	100.0	370	8	ADL18360
30	370	100.0	370	8	ADM57643
31	370	100.0	370	8	ADO20113
32	370	100.0	370	8	ADR31427
33	368	99.5	368	7	ADG65193
34	347	93.8	347	7	ADK68120
35	347	93.8	347	7	ADR49109
36	323	87.3	364	4	AAU1264
37	323	87.3	364	5	AAE15820
38	323	87.3	364	5	ABB84973
39	323	87.3	364	5	ABB95579
40	323	87.3	364	5	ABO17708
41	323	87.3	364	6	ABU80962
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57	323	87.3	364	6	ADA85662
58	323	87.3	364	6	ADA96874
59	323	87.3	364	6	ADA79178
60	323	87.3	364	6	ADA87317
61	323	87.3	364	6	ADB16519
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69	323	87.3	364	6	ADA74312
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74	323	87.3	364	6	ADA84558
75	323	87.3	364	6	ADB29814
76	323	87.3	364	6	ADA80342
77	323	87.3	364	6	ADA75584
78	323	87.3	364	6	ADA46809
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85	323	87.3	364	6	ADA96322
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87	323	87.3	364	6	ADA95770
88	323	87.3	364	6	ADB26079
89	323	87.3	364	6	ADB21564
90	323	87.3	364	7	ADA77343
91	323	87.3	364	7	ADB18083
92	323	87.3	364	7	ADA86766
93	323	87.3	364	7	ADA87869
94	323	87.3	364	7	ADA46257
95	323	87.3	364	7	ADB28287
96	323	87.3	364	7	ADB28839
97	323	87.3	364	7	ADA76791
98	323	87.3	364	7	ADA88421

99 323 87.3 364 7 ADA97426
100 323 87.3 364 7 ADB27183

ADA97426 Human PRO
ADB27183 Human PRO

ALIGNMENTS

RESULT 1

AA96864
ID AA96864 standard; protein; 370 AA.

XX AA96864;

XX 26-SEP-2000 (first entry)

DE SEQ. ID. 37 from WO0034474.

XX Vascular endothelial growth factor; homologue; zvegfg3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytoskeletal; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
KW vulnerability.

XX Homo sapiens.

XX WO200034474-A2.

XX 15-JUN-2000.

XX 07-DEC-1999; 99WO-US028968.

XX 07-DEC-1999; 98US-00207120.

XX 06-JUL-1999; 99US-0142576P.

XX 21-OCT-1999; 99US-0161653P.

XX 12-NOV-1999; 99US-0165255P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

XX Gilbertson DG, West JW;

XX WPI; 2000-423420/36.

XX N-PSDB; AAN51541.

XX Disclosure; Page 164-165; 173pp; English.

XX Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3

XX (vascular endothelial growth factor homologue) are claimed. The growth

XX factors comprise a growth factor domain and a CUB domain (generic

XX sequence motifs are shown in AA96863 and AA96860). The growth factor

XX domain is characterized by an arrangement of cysteine residues and beta-

XX strands that is characteristic of the "cysteine knot" structure of the

XX platelet-derived growth factor (PDGF) family. The CUB domain shows

XX homology to CUB domains in neuropilins, human bone morphogenetic protein-

XX 1, porcine seminal plasma protein, bovine acidic seminal fluid protein

XX and Xenopus laevis tollid-like protein. Structural analysis and homology

XX predict that ZVEGF3 polypeptides complex with a second polypeptide to

XX form multimeric proteins. The human zvegfg3 gene has been mapped to

XX chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth of

XX fibroblasts or smooth muscle cells, for activating cell surface PDGF-

XX alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular

XX processes. ZVEGF3 is useful for regulating (post-development) organ

XX growth, regeneration and maintenance, as well as tissue maintenance and

XX repair processes. ZVEGF3 antagonists are useful for treating cancer,

XX rheumatoid arthritis, diabetic retinopathy, ischemic limb disease,

XX peripheral vascular disease, myocardial ischemia, vascular intimal

XX hyperplasia, atherosclerosis, wound healing, chronic liver disease and

XX haemangioma formation. ZVEGF3 can also be used to modulate neurite growth

XX and development of the nervous system, and for treating neurodegenerative

CC diseases
XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLFFVYTLICANFCSCRDTSATPQASISAKLRANLRPESNHLTDLRRDETIOYKG 60

DB 1 MHRLFFVYTLICANFCSCRDTSATPQASISAKLRANLRPESNHLTDLRRDETIOYKG 60

QY 61 NGYVQSPRPNSYPENLLLTWRLHSEENTRIQLVFDNQFGEAEANDICRYDFVEEDIS 120

DB 61 NGYVQSPRPNSYPENLLLTWRLHSEENTRIQLVFDNQFGEAEANDICRYDFVEEDIS 120

QY 121 ETSITIRGRWCGHKEVPRIRKRTNQIKITRSDYFAKKGFKIYSLLEDFOFAASE 180

DB 121 ETSITIRGRWCGHKEVPRIRKRTNQIKITRSDYFAKKGFKIYSLLEDFOFAASE 180

QY 181 TNMESVTSISGVSNPSVTDPDLIADALDKIAEPTVBDLKYFNPESQOEDLENNY 240

DB 181 TNMESVTSISGVSNPSVTDPDLIADALDKIAEPTVBDLKYFNPESQOEDLENNY 240

QY 241 LDTPRYRGRSYHDKRSKYDLRLNDADAKRYSCTPRNYSVNIREEKLANVVFPRCLLVQ 300

DB 241 LDTPRYRGRSYHDKRSKYDLRLNDADAKRYSCTPRNYSVNIREEKLANVVFPRCLLVQ 300

QY 301 RCGNCGCGTNNMNSCTNSGKTVKHYEVQFEBGHIKRGRAKTMLVDTQLDHHERC 360

DB 301 RCGNCGCGTNNMNSCTNSGKTVKHYEVQFEBGHIKRGRAKTMLVDTQLDHHERC 360

QY 361 DCICSSRPFR 370

DB 361 DCICSSRPFR 370

RESULT 2

AA84653
ID AA84653 standard; protein; 370 AA.

XX AA84653;

XX 09-MAR-2001 (first entry)

XX Human growth factor homologue zvegfg4, SHQ ID NO:2.

XX Human; zvegfg4; growth factor homologue; VEGF/PDGF family; CUB domain;

XX PDGF-like activity; mitogenic; osteogenic; neovascularisation;

XX tissue repair; proliferation; differentiation; liver damage;

XX neurodegenerative; Alzheimer's disease; multiple sclerosis;

XX periodontal disease; bone fracture; wound healing; vulnerability; ischemia;

XX immunomodulation; hepatic; chromosome 11q22.3-23.1.

XX Homo sapiens.

XX WO200066736-A1.

XX 03-MAY-2000; 2000WO-US040047.

XX 03-MAY-1999; 99US-00304216.

XX 10-NOV-1999; 98US-0164463P.

XX 04-FEB-2000; 2000US-0180165P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX WPI; 2000-687541/67.

XX N-PSDB; AAC81555.

PT Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease.

XX Claim 1; Page 110-111; 143pp; English.

XX The invention relates to the human growth factor homologue zvegf4
XX (AA88653), and nucleic acids encoding it (AA88155). Zvegf4 is a member
XX of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
XX growth factor) family. Zvegf4 has a growth factor domain (AA88654)
XX characterised by a PDGF cysteine knot structure, and a CUB domain
XX (AA88655) which has a beta barrel structure. Zvegf4 has PDGF-like
XX activity, having mitogenic activity on fibroblasts, vascular smooth
XX muscle cells and pericytes, and has also been shown to stimulate bone
XX growth. The invention also relates to fusion proteins comprising human
XX zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
XX fusions; expression constructs and host cells comprising human zvegf4
XX nucleic acids; the recombinant expression of human zvegf4; an antibody
XX which binds to human zvegf4 or a fragment thereof; a method of activating
XX a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method
XX of modulating the proliferation, differentiation, migration or metabolism
XX of bone cells, comprising exposing bone cells to zvegf4-derived
XX polypeptides; and a method of detecting a genetic abnormality in the
XX zvegf4 gene of a patient. Zvegf4 proteins and derived fragments may be
XX used to stimulate tissue development or repair, or cellular
XX differentiation or proliferation. They are particularly used for the
XX treatment or repair of liver damage, and may also be used to modulate
XX neurite growth (e.g., in the treatment of Alzheimer's disease or multiple
XX sclerosis). Due to their osteogenic activity, they may be used in the
XX treatment of periodontal disease and fractures. They may also be used to
XX enhance expansion and mobilisation of haematopoietic stem cells and
XX endothelial precursor stem cells, which may be useful in the treatment of
XX ischaemia, in wound healing, and in the modulation of the immune system.

XX The present sequence represents human zvegf4

SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60
DB 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60
QY 61 NGVQSPRPFPNSYPRLNLLTWRLHSGQENTRIQLVFNQSGLEBAENDICRYDFEVEDIS 120
DB 61 NGVQSPRPFPNSYPRLNLLTWRLHSGQENTRIQLVFNQSGLEBAENDICRYDFEVEDIS 120
QY 121 ESTTIRGRCGCKEVPRIKSTNOIKITFKSDDFVAKRGRKIYVSLLEDPQPAASE 180
DB 121 ESTTIRGRCGCKEVPRIKSTNOIKITFKSDDFVAKRGRKIYVSLLEDPQPAASE 180
QY 181 TWNESVTSISGVSVPSTPTLADALDKKIAEFDEVEDLKKTFNPESMOEDENNY 240
DB 181 TWNESVTSISGVSVPSTPTLADALDKKIAEFDEVEDLKKTFNPESMOEDENNY 240
QY 241 LDTPRYGRSSYHDKRQVDLRLNDADAKRYSCTPRNVSVNIRELKLAVNVEPRCLLYQ 300
DB 241 LDTPRYGRSSYHDKRQVDLRLNDADAKRYSCTPRNVSVNIRELKLAVNVEPRCLLYQ 300
QY 301 RCGNGCGCTVNMRSCTCNSGKTVKYYHEVLOFEFGHFKRGRKAKTMALVDIQLDHHRC 360
DB 301 RCGNGCGCTVNMRSCTCNSGKTVKYYHEVLOFEFGHFKRGRKAKTMALVDIQLDHHRC 360
QY 361 DCICSSRPFR 370
DB 361 DCICSSRPFR 370

RESULT 3
AA71130
ID AA71130 standard; protein; 370 AA.

XX AC AA71130;
XX DT 08-SEP-2000 (first entry)
XX DE Human Platelet Derived Growth Factor (PDGF)-D protein.

XX Platelet Derived Growth Factor-D; PDGF-D; human; cytosolic; vulnery;
XX VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
XX proliferative; activator; proliferation; differentiation; motility;
XX growth; PDGF-D receptor; antagonistic; tissue remodelling; treat;
XX atherosclerosis; wound; metastasis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Domain 52..170
XX FT /label= CUB domain
XX FT /note= "Participates in protein-protein or carbohydrate
XX interactions"

FT Cleavage-site 254..257
FT /label= Proteolytic site
FT /note= "Dibasic motif"

PN MO200027879-A1.

XX 18-MAY-2000.

PF 10-NOV-1999; 99WO-US026462.

PR 10-NOV-1998; 98US-0107852P.

PR 28-DEC-1998; 98US-0113997P.

PR 26-AUG-1999; 99US-0150604P.

PR 04-OCT-1999; 99US-0157108P.

PR 05-OCT-1999; 99US-0157156P.

XX (LUDWIG-) LUDWIG INST CANCER RES.

PA (UYHR-) UNIV HELSINKI LICENSING LTD OY.

PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;

PI Oestman A, Heldin C;

DR WPI: 2000-376495/32.

DR N-PSDB; AAD00738.

XX Novel polynucleotides encoding a novel growth factor of cells expressing

PT a platelet-derived growth factor, useful for diagnostic and therapeutic

PT applications, e.g. concerning cancer.

XX Claim 25; Fig 8; 11pp; English.

XX The present sequence is the complete human platelet derived growth factor
XX (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G.
XX It is derived from human foetal lung lamdaag10 cDNA library. It belongs
XX to the VEGF/PDGF family. It functions as an activator of proliferation,
XX differentiation, growth and motility of cells, that express PDGF-D
XX receptor. This sequence is useful for inhibiting the growth of tumours,
XX that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage
XX for generating an activated truncated form is useful for regulating
XX receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for
XX inhibiting tissue remodelling during the invasion of tumour cells into
XX normal cells. PDGF-D may be used to treat wounds, atherosclerosis,
XX metastasis and migration of smooth muscle cells

SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60
DB 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIOVKG 60

```

QY 61 NGYVSPRPFPNSYPNNLLLTWRHLSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVSPRPFPNSYPNNLLLTWRHLSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRCWKCHKEVPPRIKSRITNOIKITFKSDDYFVAKGPFKIYSLLEDFOFAASE 180
Db 121 ETSIIIRGRCWKCHKEVPPRIKSRITNOIKITFKSDDYFVAKGPFKIYSLLEDFOFAASE 180
QY 181 TNWESVTSISIGVSNPSVTPDTLLADALDKKIAEPTVEDLLKYPNESPQEDLENNY 240
Db 181 TNWESVTSISIGVSNPSVTPDTLLADALDKKIAEPTVEDLLKYPNESPQEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVNIREEKLANVVFPPRCCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVNIREEKLANVVFPPRCCLLVQ 300
QY 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPFR 370
Db 361 DCICSSRPFR 370

```

RESULT 4

AAB60888
ID AAB60888 standard; protein; 370 AA.

AC AAB60888;

DT 02-APR-2001 (first entry)

DE Human VEGF-G protein.

KM Vascular endothelial growth factor; VEGF; cancer; cell; angiogenesis.

XX Homo sapiens.

OS WO200100878-A2.

PN 04-JAN-2001.

PF 29-JUN-2000; 2000WO-US018085.

PR 30-JUN-1999; 99US-00343671.

XX (MILL-) MILLENNIUM PHARM INC.

PA Gearing DP;

PI WPI; 2001-050129/06.

DR New vascular endothelial growth factor family member used for diagnosis

PT and treatment of deregulated cell growth e.g. cancer, disorders involving

PT aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases.

XX Claim 2; Fig 1; 142pp; English.

XX The present invention relates to a vascular endothelial growth factor

CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid molecules

CC are used as modulating agents or as targets for developing modulating

CC agents to regulate a variety of cellular processes e.g. cell

CC proliferation, differentiation, migration and wound repair. VEGF-G

CC modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid

CC are used to treat a subject with aberrant VEGF-G protein or nucleic acid

CC expression or activity e.g. deregulated cell growth, such as cancer,

CC hyperproliferative bone disorders, disorders involving aberrant angiogenesis

CC e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid

CC arthritis. VEGF-G gene expression is inhibited through the administration

CC of antisense molecules or ribozymes and by targeting the regulatory

CC region of VEGF-G to prevent transcription of the gene in target cells

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MHRLLFVYTLICANFCSGRDTSATPOSASIALRNANLRDESNHLTDLVRDETIQVKG 60
Db 1 MHRLLFVYTLICANFCSGRDTSATPOSASIALRNANLRDESNHLTDLVRDETIQVKG 60
QY 61 NGYVSPRPFPNSYPNNLLLTWRHLSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVSPRPFPNSYPNNLLLTWRHLSQENTRIQLVFDNFGLEAEANDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRCWKCHKEVPPRIKSRITNOIKITFKSDDYFVAKGPFKIYSLLEDFOFAASE 180
Db 121 ETSIIIRGRCWKCHKEVPPRIKSRITNOIKITFKSDDYFVAKGPFKIYSLLEDFOFAASE 180
QY 181 TNWESVTSISIGVSNPSVTPDTLLADALDKKIAEPTVEDLLKYPNESPQEDLENNY 240
Db 181 TNWESVTSISIGVSNPSVTPDTLLADALDKKIAEPTVEDLLKYPNESPQEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVNIREEKLANVVFPPRCCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYDLDRINDAKRYSCTPRNYSVNIREEKLANVVFPPRCCLLVQ 300
QY 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGGTVMNRSCCTNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPFR 370
Db 361 DCICSSRPFR 370

```

RESULT 5

AAU00704
ID AAU00704 standard; protein; 370 AA.

AC AAU00704;

DT 07-SEP-2001 (first entry)

DE Human PDGFR protein.

KM Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;

KM VEGF-E; platelet derived growth factor; PDGF; FGF; hyperplasia; cancer;

KM neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;

KM fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;

KM dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;

KM inflammatory disorder; Graft versus host disease; coagulation;

KM haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;

KM multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;

XX peripheral neuropathy; acute brain injury.

XX Homo sapiens.

OS WO200125437-A2.

PN 12-APR-2001.

PF 06-OCT-2000; 2000WO-US027671.

PR 07-OCT-1999; 99US-0158083P.

PR 13-OCT-1999; 99US-0159231P.

PR 04-JAN-2000; 2000US-0174485P.

PR 03-MAR-2000; 2000US-0186707P.

PR 10-MAR-2000; 2000US-0188250P.

PR 08-AUG-2000; 2000US-0223879P.

PR 12-SEP-2000; 2000US-0066278P.

PR 20-SEP-2000; 2000US-0234082P.

PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
 PI Jeffers M;
 XX
 DR WPI; 2001-316172/33.
 DR N-PSDB; AAS04498.
 XX
 PT Novel growth factor polypeptides termed as FCTR polypeptides, useful for
 PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
 PT wound healing and neuronal disorders.
 XX
 PS Disclosure; Fig 13: 171pp; English.
 XX
 CC The sequence represents a protein related to bone morphogenetic protein-1
 CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
 CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
 CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
 CC FCTR proteins are useful for treating or preventing a disorder
 CC associated with aberrant expression, aberrant processing, or aberrant
 CC physiological interactions of the proteins in a mammal, where the
 CC disorder is characterised by insufficient or ineffective growth of a cell
 CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
 CC associated nucleic acids are useful for both promoting and inhibiting
 CC growth of cells and tissues and in treatment of cancer, anaemia,
 CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
 CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
 CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC inflammatory disorders, graft versus host disease, coagulation disorders
 CC such as haemophilia, and neural disorders including Parkinson's disease,
 CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
 CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
 CC and epilepsy
 CC
 XX
 SQ Sequence 370 AA;
 Query Match 100.0%; Score 370; DB 4; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAU00698;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human FCTR1 protein present in clone 30664188.0.99.
 XX
 KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
 KW VEGF-E; platelet derived growth factor; PDGF; FCTR; hyperplasia; cancer;
 KW neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
 KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
 KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
 KW inflammatory disorder; Graft versus host disease; coagulation;
 KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
 KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
 KW peripheral neuropathy; acute brain injury.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /note="Signal peptide"
 FT Protein 24..370
 FT /note="Mature FCTR1"
 FT Domain 53..167
 FT /note="CUB domain"
 FT Domain 272..306
 FT /note="PDGF domain"
 FT Modified-site 276
 FT /note="N-linked glycosylation site"
 FT Domain 302..365
 FT /note="Metallothionein domain"
 FT Domain 350..362
 FT /note="PDGF domain"
 FT
 XX
 PN WO200125437-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US027671.
 XX
 XX 07-OCT-1999; 99US-0158083P.
 PR 13-OCT-1999; 99US-0159231P.
 PR 04-JAN-2000; 2000US-0174485P.
 PR 03-MAR-2000; 2000US-0186707P.
 PR 10-MAR-2000; 2000US-0188250P.
 PR 08-AUG-2000; 2000US-0223879P.
 PR 12-SEP-2000; 2000US-00662783.
 PR 20-SEP-2000; 2000US-0234082P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
 PI Jeffers M;
 XX
 DR WPI; 2001-316172/33.
 DR N-PSDB; AAS04498.
 XX
 PT Novel growth factor polypeptides termed as FCTR polypeptides, useful for
 PT treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
 PT wound healing and neuronal disorders.
 XX
 PS Claim 1; Fig 1; 171pp; English.
 XX
 CC The sequence represents a protein related to bone morphogenetic protein-1
 CC (BMP-1), vascular endothelial growth factor (VEGF-E) and platelet derived
 CC growth factor (PDGF). Polypeptides and polynucleotides related to BMP-1,
 CC VEGF-E and PDGF are referred to as FCTR polypeptides and nucleic acids.
 CC FCTR proteins are useful for treating or preventing a disorder
 CC associated with aberrant expression, aberrant processing, or aberrant
 CC physiological interactions of the proteins in a mammal, where the
 CC disorder is characterised by insufficient or ineffective growth of a cell
 CC or a tissue, e.g. hyperplasia or neoplasia. The peptides and their
 CC associated nucleic acids are useful for both promoting and inhibiting

CC growth of cells and tissues and in treatment of cancer, anaemia,
 CC leukopenia, baldness, for treating cardiovascular and fibrotic disorders,
 CC diabetic ulcers, obesity, infectious diseases, hyperproliferative and
 CC dysproliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC inflammatory disorders, graft versus host disease, coagulation disorders
 CC such as haemophilia, and neural disorders including Parkinson's disease,
 CC Alzheimer's disease, multiple sclerosis, Huntington's disease,
 CC amyotrophic lateral sclerosis, peripheral neuropathy, acute brain injury
 CC and epilepsy

XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
 DB 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
 QY 61 NGYVQSPFPNSYPNNLLTWRHLSOENTRIQLVFDNFGLEAENDICRYDFVEVEDIS 120
 DB 61 NGYVQSPFPNSYPNNLLTWRHLSOENTRIQLVFDNFGLEAENDICRYDFVEVEDIS 120
 QY 121 ETSITIRGMCQHKVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLBDFQPAASE 180
 DB 121 ETSITIRGMCQHKVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLBDFQPAASE 180
 QY 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEPTVEDLLKYFNPESQOELENNY 240
 DB 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEPTVEDLLKYFNPESQOELENNY 240
 QY 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNIREBEIKLANVVFPPCLLVQ 300
 DB 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNIREBEIKLANVVFPPCLLVQ 300
 QY 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
 DB 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
 QY 361 DCICSSRPPR 370
 DB 361 DCICSSRPPR 370

RESULT 7

AAG65601 ID AAG65601 standard; protein; 370 AA.

XX AAG65601;

DT 07-JAN-2002 (first entry)

XX Human zvegfg4 polypeptide.

XX zvegfg4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;
 KW bone cancer; osteonecrosis; bone defect; osteogenesis; osteoporosis;
 KW osteopathic; vulnery; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..18 /note= "secretory peptide"

FT Protein 19..370 /note= "mature protein"

FT Domain 52..179 /note= "CUB domain"

FT Region 180..257 /note= "propeptide-like sequence"

FT Domain 258..370 /note= "growth factor domain"

XX

PN W0200157083-A1.
 XX 09-AUG-2001.
 PD 03-MAY-2000; 2000WO-US012095.
 XX 04-FEB-2000; 2000US-0180169P.
 PR 31-MAR-2000; 2000US-00540224.
 XX (ZYMO) ZYMOGENETICS INC.

XX Gilbertson DG, Hart CE;

XX WPI; 2001-611088/70.

DR N-PSDB; AAH47772.

PT Use of zvegfg4 polypeptide for promoting bone, ligament or cartilage
 PT growth in mammal at site of fracture, implant, and bone graft, and for
 PT promoting growth or differentiation of osteoblasts, chondrocytes in
 PT culture.

XX Example 2; Page 44-47; 57p; English.

CC The invention relates to the use of zvegfg4 polypeptide for promoting
 CC bone, ligament or cartilage growth in a mammal, and for promoting
 CC proliferation or differentiation of osteoblasts, osteoclasts,
 CC chondrocytes or bone marrow stem cells in culture. For promoting
 CC cartilage growth, chondrocytes are cultured ex vivo in presence of the
 CC zvegfg4 polypeptide and then placed into mammal where cartilage is to be
 CC grown. Zvegfg4 polypeptide is useful for promoting growth of bone,
 CC ligament or cartilage in a mammal at a site of bony defect such as
 CC fracture, bone graft, implant or periodontal pocket, in humans and non-
 CC human animals such as domestic animals including livestock and companion
 CC animals. Zvegfg4 is used for promoting growth of bone, ligament, or
 CC cartilage in conditions of bone defects following therapeutic treatments
 CC of bone cancers or other conditions characterized by increased bone loss
 CC or decreased bone formation, or elevation of peak bone mass in pro-
 CC menopausal woman. It is also useful for healing bone following radiation
 CC induced osteonecrosis, repairing bone defects arising from surgery, and
 CC promotion of bone healing in plastic surgery, increasing bone formation
 CC during distraction osteogenesis, treating bone injuries including repair
 CC of cartilage and ligament and treatment of osteoporosis. The present
 CC sequence represents a human zvegfg4 polypeptide

XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
 DB 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETIQYKG 60
 QY 61 NGYVQSPFPNSYPNNLLTWRHLSOENTRIQLVFDNFGLEAENDICRYDFVEVEDIS 120
 DB 61 NGYVQSPFPNSYPNNLLTWRHLSOENTRIQLVFDNFGLEAENDICRYDFVEVEDIS 120
 QY 121 ETSITIRGMCQHKVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLBDFQPAASE 180
 DB 121 ETSITIRGMCQHKVPPRIKSRITNOIKITPKSDDYFVAKPGFKIYYSLLBDFQPAASE 180
 QY 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEPTVEDLLKYFNPESQOELENNY 240
 DB 181 TNWESVTSISGVSNSSVTDPTLIADALDKKIAEPTVEDLLKYFNPESQOELENNY 240
 QY 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNIREBEIKLANVVFPPCLLVQ 300
 DB 241 LDTPRYGRSYHDKRSKYVDLRLNDAKRYSCTPRNYSVNIREBEIKLANVVFPPCLLVQ 300
 QY 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360
 DB 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEBGHIKRRGRAKTMALVDIQLDHHERC 360

Oy	361	DCICSSRPPR 370
Db	361	DCICSSRPPR 370
RESULT 8		
AAE00999		
AAE00999	standard; protein; 370 AA.	
AAE00999;		
04-JUL-2001	(first entry)	
Human Zvegfg4 protein which forms heteromultimer with Zvegfg3 protein.		
Human; Zvegfg3 antagonist; cell proliferation; stellate cell activation; extracellular matrix production; fibrosis; VEGF-R; PDGF-C; platelet-derived growth factor; PDGF; vascular endothelial growth factor; VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder; chronic active hepatitis; fulminant viral hepatitis; amyloidosis; diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis; asbestosis; renal arteriosclerosis; post necrotic cirrhosis; diabetic glomerulosclerosis; focal glomerulosclerosis; hypertostosis; pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis; bronchiolitis obliterans-organising pneumonia; transplant vasculopathy; fibroproliferative disorder; Zvegfg4 protein.		
Homo sapiens.		
MO200128586-A1.		
26-APR-2001.		
23-OCT-2000; 2000MO-US029270.		
21-OCT-1999; 99US-0161653P.		
12-NOV-1999; 99US-0165255P.		
01-AUG-2000; 2000US-0222223P.		
(ZVMO) ZYMOGENETICS INC.		
Gilbertson DG;		
WPI; 2001-300278/31.		
Use of zvegfg3 antagonist for reducing fibroproliferative disorder of kidney, liver and bone, reducing extracellular matrix production, treating fibrosis or reducing stellate cell activation in mammal.		
Disclosure; Page 62-63; 70pp; English.		
The patent discloses materials and methods for reducing cell proliferation or extracellular matrix production, treating fibrosis and reducing stellate cell activation in a mammal. The method comprises administering a composition containing a Zvegfg3 antagonist in combination with a delivery vehicle. The Zvegfg3 is a protein that is structurally related to platelet-derived growth factor (PDGF) and the vascular endothelial growth factors (VEGF). The Zvegfg3 protein is also designated as "VEGF-R" and "PDGF-C". The Zvegfg3 antagonist is useful to block the mitogenic effects of zvegfg3 and thereby to inhibit or prevent and treat keloid, scleroderma, fibrotic disorders of liver such as chronic active hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis, bronchiolitis obliterans-organising pneumonia and pulmonary hypertension, fibrotic disorders of pancreas, fibroproliferative disorders of the vasculature such as transplant vasculopathy and fibroproliferative disorders of the bone such as osteopetrosis and hyperostosis. The present sequence is human Zvegfg4 protein which forms a heteromultimer with Zvegfg3 protein.		

XX	Sequence	370 AA;
SQ	Query Match	100.0%; Score 370; DB 4; Length 370;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 370; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1	MHRLLFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLVRRDETIOVGK 60
Dd	1	MHRLLFVYTLICANFCSCRDTSATPQSASIKALRNANLRDESNHLTDLVRRDETIOVGK 60
OY	61	NGYVQSPFPNSYPNNLLLTWRLHSEOENTRIQLVFNDQGLEEAENDICRYDFVEVEDIS 120
Dd	61	NGYVQSPFPNSYPNNLLLTWRLHSEOENTRIQLVFNDQGLEEAENDICRYDFVEVEDIS 120
OY	121	ETSTTIIRRMCGKHKEVPPIRKSRTNQKITTFKSDDYFVAKPGFKIYSLLEDPQPAASE 180
Dd	121	ETSTTIIRRMCGKHKEVPPIRKSRTNQKITTFKSDDYFVAKPGFKIYSLLEDPQPAASE 180
OY	181	TNMEVSVTSSIGSVSYNSPSVTDPTLIADALDKIAEFDVEDLTKVFNESEQEDLENMY 240
Dd	181	TNMEVSVTSSIGSVSYNSPSVTDPTLIADALDKIAEFDVEDLTKVFNESEQEDLENMY 240
OY	241	LDTPRYRGSRSHDRKSKVDLDRLANDAKRYSGTPPNYSVINREBELKANVFFPRCLLVQ 300
Dd	241	LDTPRYRGSRSHDRKSKVDLDRLANDAKRYSGTPPNYSVINREBELKANVFFPRCLLVQ 300
OY	301	RGGGCGCGGTVMNRCTCNSGKTVKKYHEVLQFEFGHIKRGRAKTMALVDIQLDHHERC 360
Dd	301	RGGGCGCGGTVMNRCTCNSGKTVKKYHEVLQFEFGHIKRGRAKTMALVDIQLDHHERC 360
OY	361	DCICSSRPFR 370
Dd	361	DCICSSRPFR 370
RESULT 9		
ID	AAB85529	standard; protein; 370 AA.
AC	AAB85529;	
XX	25-SEP-2001	(first entry)
De	Human secreted protein (clone Id HGNC48).	
KW	Secreted protein; immunosuppressive; antiarthritic; antirheumatic;	
KM	antiapoptotic; cytostatic; cardiant; vasotropic; cerebroprotective;	
XX	neurotrophic; neuroprotective; antibacterial; virucide; fungicide; human;	
OS	ophthalmological; gene therapy.	
XX	Homo sapiens.	
XX	WO200155430-A1.	
PD	02-AUG-2001.	
XX	17-JAN-2001; 2001WO-US001431.	
XX	31-JAN-2000; 2000US-0179065P.	
PR	04-FEB-2000; 2000US-0180628P.	
PR	12-SEP-2000; 2000US-0231968P.	
XX	(HUMA-) HUMAN GENOME SCT INC.	
XX	Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;	
PI	Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;	
PI	Fiscella M, Ni J, Ruben SM, Barash SC;	
XX	WPI; 2001-476220/51.	
DR	N-PSDB; AAH46939.	
XX	17 isolated nucleic acid molecules encoding human secreted proteins, used	

PT to preventing, treating or ameliorating a medical condition.
XX
PS Claim 11; Page 447-449; 482pp; English.

CC The invention provides novel human secreted proteins and polynucleotides
CC encoding them. The secreted proteins can be expressed by standard
CC recombinant methodology. The secreted proteins and polynucleotides are
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
CC also be used in diagnosing a pathological condition. The antibodies to
CC the proteins can also be used in alleviating symptoms associated with the
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. The present
CC sequence represents a human secreted protein

XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPQASISALANANRRDSEHNLDTLYRDETIOYKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPQASISALANANRRDSEHNLDTLYRDETIOYKG 60
QY 61 NGYVSPFPFNSYPRLNLLTWRHLSOENTRIQVFNQFGLAEANDICRYDFVEVEDIS 120
DB 61 NGYVSPFPFNSYPRLNLLTWRHLSOENTRIQVFNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
QY 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEPFTVBDLKYFNPESQOELENNY 240
DB 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEPFTVBDLKYFNPESQOELENNY 240
QY 241 LDTPRYGRSRYHDKRSKYDLRLNDADAKRYSCTPRNYGVNIIEELKLANVVFPPRCLLVQ 300
DB 241 LDTPRYGRSRYHDKRSKYDLRLNDADAKRYSCTPRNYGVNIIEELKLANVVFPPRCLLVQ 300
QY 301 RCGNGCGCGTVNMSCTCNSGKTVKKYHEVLOFEPGHIRKGRAKTMALVLDIOLDHHERC 360
DB 301 RCGNGCGCGTVNMSCTCNSGKTVKKYHEVLOFEPGHIRKGRAKTMALVLDIOLDHHERC 360
QY 361 DCICSRPPR 370
DB 361 DCICSRPPR 370

RESULT 10

AAE15819
ID AAE15819 standard; protein; 370 AA.

XX AAE15819;

XX 26-MAR-2002 (first entry)

XX Human LP85 protein #1.

XX LP85; platelet-derived growth factor; PDGF; antiinflammatory; vulnerary;
KW osteopathic; neuroprotective; tranquilliser; musculoskeletal disorder;

KW MSD; therapy; bone growth; cartilage differentiation; wound healing;
KW neuron growth; bone fracture; osteoporosis; osteopenia; arthritis;
KW sarcopenia; periodontal disease; tissue atrophy; endocrine disorder;
KW muscle loss; immobility; bone density.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..12
FT /label= Signal_peptide
FT Protein 13..370
FT /label= Human_mature_LP85_protein

PN WO200189450-A2.

PD 29-NOV-2001.

XX 08-MAY-2001; 2001WO-US011755.

XX 19-MAY-2000; 2000US-0205424P.

PR 11-JAN-2001; 2001US-0261071P.

PR 11-JAN-2001; 2001US-0261076P.

XX (BIL) LILLY & CO ELI.

XX Beals JM, Gonzalez-Dewhite PA, Hammond LJ, Lu J, Na S, Su EW;
PI Witcher DR, Wroblewski VJ;

XX WPI; 2002-083040/11.

DR N-PSDB; AAD15819.

PT Analog of a platelet-derived growth factor homolog, LP85 useful for
PT treating osteoporosis, arthritis, sarcopenia, wounds, has one or more
PT amino acid substitutions which destroy the tripeptidyl sequence of native
PT LP85.

XX Claim 11; Page 109-110; 117pp; English.

XX The present invention relates to LP85, an analogue of platelet-derived
XX growth factor (PDGF) homologue. Sequences of the invention are useful for
XX the manufacture of a medicament for treating musculoskeletal disorder
XX (MSD) which include promoting bone growth, cartilage differentiation and
XX function, wound healing, neuron growth, preventing cartilage degradation
XX or neuronal degeneration. They are useful for treating bone fractures,
XX osteoporosis, osteopenia, arthritis, sarcopenia, periodontal disease,
XX tissue atrophy, traumatised connective tissues, grafted connective
XX tissues and/or transplanted organs, bone or muscle loss due to
XX malignancy, endocrine disorders and immobility. They are also used for
XX prophylactically increasing or maintaining bone density in a mammal. The
XX present sequence is human LP85 protein

XX Sequence 370 AA;

Query Match 100.0%; Score 370; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPQASISALANANRRDSEHNLDTLYRDETIOYKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPQASISALANANRRDSEHNLDTLYRDETIOYKG 60
QY 61 NGYVSPFPFNSYPRLNLLTWRHLSOENTRIQVFNQFGLAEANDICRYDFVEVEDIS 120
DB 61 NGYVSPFPFNSYPRLNLLTWRHLSOENTRIQVFNQFGLAEANDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNQIKITFKSDDYFVAKPGFKIYSLLEDFOPAASE 180
QY 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEPFTVBDLKYFNPESQOELENNY 240
DB 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEPFTVBDLKYFNPESQOELENNY 240

Pf		07-DEC-1999;	99US-00457066.	
Px		07-DEC-1998;	98US-0111173P.	
Px		06-JUL-1999;	99US-0142576P.	
Pr		21-OCT-1999;	99US-0161653P.	
Px		12-NOV-1999;	99US-0165255P.	
Ra	(ZYMO) ZYMOGENETICS INC.			
Pi	Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;			
Pi	Gilbertson DG, West JW;			
Dx	MPI: 2002-689759/74.			
Dr	N-PSDB; ABS68643.			
Pt	Novel polypeptide, designated zvegf3 useful for treating skin wounds,			
Pt	ulcers, burns, skin grafting, female reproductive tract disorders,			
Pt	Parinson's disease, and Alzheimer's disease.			
Px				
Ps	Disclosure; Col 95-98; 68pp; English.			
Cc				
Cc	The invention relates to an isolated polypeptide, designated zvegf3 (a			
Cc	vascular endothelial growth factor-like protein) of 11-136 amino acid			
Cc	residues in length and comprises the sequence appearing as AAG92889 from			
Cc	amino acid residues 235-345. Also included are an isolated protein			
Cc	comprising a first polypeptide disulphide bonded to a second polypeptide,			
Cc	where each of the first and second polypeptides is from zvegf 3, and			
Cc	where the protein modulates cell proliferation, differentiation,			
Cc	metabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3			
Cc	expression vectors and host cells. Zvegf 3 is useful as additives in			
Cc	tissue adhesives for promoting revascularisation of the healing tissue,			
Cc	for designing molecules that antagonise semaphorin-stimulated activities,			
Cc	including neurite growth, cardiovascular development, cartilage and limb			
Cc	development, and T and B-cell function, and for imaging tumours or other			
Cc	sites of abnormal cell proliferation and in gene therapy applications.			
Cc	The proteins are useful therapeutically to stimulate tissue development			
Cc	or repair, or cellular differentiation or proliferation, for stimulating			
Cc	the growth of fibroblast or smooth muscle cells, as molecular weight			
Cc	standards, as reagents in assays for determining circulatory level of the			
Cc	protein or as standards in the analysis of cell phenotype, for			
Cc	identifying inhibitors of their activity which are useful for reducing			
Cc	the growth of solid tumours, for treating diabetic retinopathy,			
Cc	psoriasis, rheumatoid arthritis, various forms of cancers, autoimmune			
Cc	disease, inflammation, myocardial ischaemia, scleroderma, and reducing			
Cc	fibrosis, including scar formation, keloids, liver fibrosis, lung			
Cc	fibrosis (e.g. silicosis, asbestosis), kidney fibrosis (including			
Cc	diabetic nephropathy), glomerulosclerosis, atherosclerosis, skin wounds,			
Cc	ulcers, burns, skin grafting, and female reproductive tract disorders,			
Cc	chronic liver disease (hepatitis), cirrhosis, Reye's syndrome, Wilson's			
Cc	disease, circulatory disorders e.g. heart failure, hepatic or portal vein			
Cc	thrombosis, cardiac sclerosis, neurodegenerative diseases such as			
Cc	multiple sclerosis, Parkinson's disease, Alzheimer's disease, and for			
Cc	regenerating neurite outgrowths following strokes. The gene for human			
Cc	zvegf3 is located on chromosome 4q28.3. The present sequence represents			
Cc	zvegf 3			
SQ				
SQ	Sequence 370 AA:			
	Query Match	100.0%;	Score 370;	DB 5; Length 370;
	Best Local Similarity	100.0%;	Pred No. 0;	
	Matches 370;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0
Oy	1 MHRLLFFVTLLICANCSGCRDTSATPOASISIKLRNRNLRDESNHLDLYRRDETQVKG 60			
Db	1 MHRLLFFVTLLICANCSGCRDTSATPOASISIKLRNRNLRDESNHLDLYRRDETITQVGK 60			
Oy	61 NGYVSPPFPNSYPNNLLTWRLHSQEENTRIQLVFNDNGFLEEAENDICRYDFVEVEDIS 120			
Db	61 NGYVSPPFPNSYPNNLLTWRLHSQEENTRIQLVFNDNGFLEEAENDICRYDFVEVEDIS 120			
Oy	121 ETSIIIRGRWGHKEVPRIKSRTNQIKTFESDDYFAAKPEFKIYYSLLEDFOGPAASE 180			
Db	121 ETSIIIRGRWGHKEVPRIKSRTNQIKTFESDDYFAAKPEFKIYYSLLEDFOGPAASE 180			

Qy	161	TWNEVSTSSISGVSNVNSVYDPTLIALDALDKKIAEFVPEVDLKKFNENSOQEDLENNY	240
Db	161	TWNEVSTSSISGVSNVNSVYDPTLIALDALDKKIAEFVPEVDLKKFNENSOQEDLENNY	240
Qy	241	LDTPPYRGRSVHYDRSKSYVDLDRLNDADAKRYSCTPRNYSVINIREELKLAVVFFPRCLLVQ	300
Db	241	LDTPPYRGRSVHYDRSKSYVDLDRLNDADAKRYSCTPRNYSVINIREELKLAVVFFPRCLLVQ	300
Qy	301	RCGNGCGGTVMWRECTCNSGKTVKKYHEVLQPEPGHIKRRGRAKTMALVDIOLDHHERC	360
Db	301	RCGNGCGGTVMWRECTCNSGKTVKKYHEVLQPEPGHIKRRGRAKTMALVDIOLDHHERC	360
Qy	361	DCICSSRPFR 370	
Db	361	DCICSSRPFR 370	
RESULT 13			
AAB47891			
ID	AAB47891 standard; protein; 370 AA.		
AC	AAB47891;		
XX			
DT	16-MAY-2002 (first entry)		
XX			
DE	Human zvegfg4.		
XX			
KW	Human; mouse; zvegfg3; zvegfg4; platelet derived growth factor; PDGF;		
KW	homolog; growth; bone; ligament; cartilage; proliferation; osteoblast;		
KW	chondrocyte; bony defect; fracture; bone graft; implant;		
KW	periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.		
XX			
OS	Homo sapiens.		
XX			
PN	US2002004225-A1.		
XX			
PD	10-JAN-2002.		
XX			
PF	29-MAR-2001; 2001US-00823033.		
XX			
PR	07-DEC-1998; 98US-0111173P.		
PR	06-JUL-1999; 99US-0142576P.		
PR	21-OCT-1999; 99US-0161653P.		
PR	12-NOV-1999; 99US-0165255P.		
PR	07-DEC-1999; 99US-00457066.		
PR	31-MAR-2000; 2000US-0193723P.		
XX			
PA	(HART/) HART C E.		
XX			
PA	(GILB/) GILBERTSON D G.		
XX			
PI	Hart CE, Gilbertson DG;		
XX			
DR	WPI; 2002-171026/22.		
XX			
PT	Promoting growth of bone, ligament or cartilage in a mammal, involves		
PT	administering to the mammal a protein which comprises growth factor		
PT	domain of zvegfg3 protein, a homolog of platelet-derived growth factor.		
XX			
PS	Claim 8, Page 20-21; 31pp; English.		
XX			
XX			

Cy 301 RCGNCGCGTNNMRSCTCNSGKTVKKEHYEVLOFEPGHIKKRGRAKTMALVDIQLDHHERC 360
| | | | |
Db 301 RCGNCGCGTNNMRSCTCNSGKTVKKEHYEVLOFEPGHIKKRGRAKTMALVDIQLDHHERC 360
| | | | |
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370
| | | | |

RESULT 15

ABG78502
ID ABG78502 standard; protein; 370 AA.
XX
AC ABG78502;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human FCTR 1 protein.
XX
KW 3066418 antigen; blood; cancer; human; FCTR.
XX
OS Homo sapiens.
XX
PN WO200259618-A2.
XX
PD 01-AUG-2002.
XX
PF 16-NOV-2001; 2001WO-US048901.
XX
PR 16-NOV-2000; 2000US-00715332.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkovs RA, Lichenstein H, Herrmann JL, Boldog FL, Minskoff S;
PI Jeffers M, Andrews D, Larochele W;
XX
DR MPI; 2002-619187/66.
XX
N-PSDB; ABS63515.

PT Detecting presence or amount of 3066418 antigen in a sample, by
PT contacting the biological sample with agent that binds the antigen, and
PT detecting the presence or amount of agent bound to the antigen.

Example 1; Page 11-13; 177pp; English.

CC The present invention relates to a new method of detecting the presence
CC of 3066418 antigen in a sample. The invention is useful for detecting
CC the presence of 3066418 in a biological sample (e.g. blood or its
CC component originating from a mammal, preferably human), and for
CC contributing to diagnosis of cancer in a subject. The present amino acid
CC sequence represents a human FCTR protein, as described in the methods of
CC the invention
XX
XX

Sequence 370 AA;

Query Match 100.0%; Score 370; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSCRDTSATPQASIKALRNANLRDSENLTLDRDETIOVKG 60
| | | | |
Db 1 MHRLLFYVTLICANFCSCRDTSATPQASIKALRNANLRDSENLTLDRDETIOVKG 60
| | | | |
Qy 61 NGYVOSPPFPNSYPNNLLTLWRHLSQENTRIOLVFDNQGFLBEANDICRYDFEVEDIS 120
| | | | |
Db 61 NGYVOSPPFPNSYPNNLLTLWRHLSQENTRIOLVFDNQGFLBEANDICRYDFEVEDIS 120
| | | | |
Qy 121 ESTTIRGRCGCHKVFPRIKSRITQIKITFKSDYFPAKPGFKIYYSLLEDFOPAAASE 180
| | | | |
Db 121 ESTTIRGRCGCHKVFPRIKSRITQIKITFKSDYFPAKPGFKIYYSLLEDFOPAAASE 180
| | | | |
Qy 181 TNWESVTSSISGVSYNSPSVTDFTLIADALDKIAEFDTVEDLLKYNPESWQEDLENNY 240
| | | | |

Db 181 TNWESVTSSISGVSYNSPSVTDFTLIADALDKIAEFDTVEDLLKYNPESWQEDLENNY 240
| | | | |
Qy 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCTRPNYSVNIREEIKLANVVFPPRCILVO 300
| | | | |
Db 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCTRPNYSVNIREEIKLANVVFPPRCILVO 300
| | | | |
Qy 301 RCGNCGCGTNNMRSCTCNSGKTVKKEHYEVLOFEPGHIKKRGRAKTMALVDIQLDHHERC 360
| | | | |
Db 301 RCGNCGCGTNNMRSCTCNSGKTVKKEHYEVLOFEPGHIKKRGRAKTMALVDIQLDHHERC 360
| | | | |
Qy 361 DCICSSRPPR 370
| | | | |
Db 361 DCICSSRPPR 370
| | | | |

RESULT 16

ABG76575
ID ABG76575 standard; protein; 370 AA.
XX
AC ABG76575;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human secreted protein #7.
XX
KW Human; secreted protein; autoimmune disease; blood coagulation disorder;
KW blood platelet disorder; hyperproliferative disorder; renal disorder;
KW neurodegenerative disorder; cardiovascular disorder; vascular disorder;
KW respiratory disorder; endocrine disorder; reproductive disorder;
KW gastrointestinal disorder; infectious disease; antidiabetic; cytostatic;
KW antiarthritic; immunosuppressive; antiasclerotic; antidiabetic;
KW antiinflammatory; antipsoriatic; antiparkinsonian; neuroprotective.
XX
XX

OS Homo sapiens.
XX
PN US2002120103-A1.
XX
PD 29-AUG-2002.
XX
PF 27-JUL-2001; 2001US-00915582.
XX
PR 31-JAN-2000; 2000US-0179065P.
XX
PR 04-FEB-2000; 2000US-0180628P.
XX
PR 12-SEP-2000; 2000US-0231968P.
XX
PR 17-JAN-2001; 2001WO-US001431.
XX

XX (ROSE/) ROSEN C A.
XX (KOMA/) KOMATSUJIS G A.
XX (BAKE/) BAKER K P.
XX (BIRS/) BIRSE C E.
XX (SOPR/) SOPPET D R.
XX (ORSE/) OLSEN H S.
XX (MOOR/) MOORE P A.
XX (WEIP/) WEI P.
XX (EBNE/) EBNER R.
XX (DUAN/) DUAN D R.
XX (SHIY/) SHI Y.
XX (CHOI/) CHOI G H.
XX (FISC/) FISCELLA M.
XX (NIJU/) NI J.
XX (RUBEN/) RUBEN S M.
XX (BARA/) BARASH S C.

XX (BARA/) BARASH S C.
XX
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
XX Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
XX Fiscella M, Ni J, Ruben SM, Barash SC;
XX

XX MPI; 2002-608160/65.
XX N-PSDB; ABS58475.
XX
XX New secreted polypeptides and encoding polynucleotides, useful for
XX preventing, treating and diagnosing diseases e.g. anemia, cancer,
XX

PT diabetes, asthma, psoriasis, Parkinson's and Alzheimer's.
 XX
 XX Claim 11: Page 389-390; 238pp; English.
 CC The invention relates to an isolated nucleic acid molecule which encodes
 CC a human secreted protein. The sequences are useful for diagnosing or
 CC diagnosing a susceptibility to a pathological condition in a subject
 CC comprising determining the presence or absence of a mutation in the DNA
 CC or expression of the protein. The sequences are useful for identifying a
 CC binding partner to the protein comprising contacting the protein with a
 CC binding partner and determining whether the binding partner effects an
 CC activity. The DNA and protein sequences are used for preventing, treating
 CC or ameliorating a medical condition such as an autoimmune disease (e.g.
 CC multiple sclerosis, myasthenia gravis), blood coagulation disorders (e.g.
 CC afibrinogenemia, haemophilia), blood platelet disorders (e.g.
 CC thrombocytopenia), hyperproliferative disorders (e.g. sarcoidosis, Sezary
 CC syndrome), neurodegenerative disorders (e.g. Alzheimer's disease,
 CC Parkinson's disease), renal disorders (e.g. renal vein thrombosis, kidney
 CC infection), cardiovascular disorders (e.g. cardiac arrest,
 CC pericarditis), vascular disorders (e.g. aneurysm, ischaemia), respiratory
 CC disorders (e.g. tonsillitis, laryngitis), endocrine disorders (e.g.
 CC acromegaly, thyrotoxicosis), reproductive disorders (gonorrhea,
 CC stenosis), gastrointestinal disorders (e.g. gastroenteritis, pyloric
 CC stenosis), infectious diseases (e.g. polio, rubella) and cancer.
 CC Sequences ABG76569-ABG76616 represent human secreted proteins of the
 CC invention
 XX
 XX Sequence 370 AA;
 SQ
 Query Match 100.0%; Score 370; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDSENLTDLYRDETTQVKG 60
 DB 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDSENLTDLYRDETTQVKG 60
 QY 61 NGVOSPRFPNSYPRLNLTWRLHSEONTRIQLVFNQGLEBAENDICRYDVEVEDIS 120
 DB 61 NGVOSPRFPNSYPRLNLTWRLHSEONTRIQLVFNQGLEBAENDICRYDVEVEDIS 120
 QY 121 ESTTIIRGRWCGHKEVPRIKSRITNOIKITPKSDYFVAKPGFKIYYSLLDEFPQAAASE 180
 DB 121 ESTTIIRGRWCGHKEVPRIKSRITNOIKITPKSDYFVAKPGFKIYYSLLDEFPQAAASE 180
 QY 181 TNWESVTSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKTFNPESQEDLENNY 240
 DB 181 TNWESVTSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKTFNPESQEDLENNY 240
 QY 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVNIIRBELKLANVFFPRCLLVQ 300
 DB 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVNIIRBELKLANVFFPRCLLVQ 300
 QY 301 RCGNGCGCTVWNRSCCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360
 DB 301 RCGNGCGCTVWNRSCCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360
 QY 361 DCTCSSRPPR 370
 DB 361 DCTCSSRPPR 370
 RESULT 17
 ABG64733 ID ABG64733 standard; protein; 370 AA.
 XX AC ABG64733;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human albumin fusion protein #1408.
 XX
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;

KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antineoplastic; antiinflammatory; anticler;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nocotropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200177137-A1.
 XX
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US011988.
 XX
 PR 12-APR-2000; 2000US-0229358P.
 PR 25-APR-2000; 2000US-0199384P.
 PR 21-DEC-2000; 2000US-0256931P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Haseltine WA;
 XX
 DR WPI, 2002-010886/01.
 XX
 PT New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein.
 XX
 PS Claim 1; Page 1459-1460; 2102pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or disorder
 CC that may be modulated by therapeutic protein X. The albumin extends the
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo
 CC activity. The protein is useful for treating and diagnosing disorders
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
 CC disease, ulcerative colitis), immune disorders (e.g. acquired
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
 XX
 XX Sequence 370 AA;
 SQ
 Query Match 100.0%; Score 370; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDSENLTDLYRDETTQVKG 60
 DB 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDSENLTDLYRDETTQVKG 60
 QY 61 NGVOSPRFPNSYPRLNLTWRLHSEONTRIQLVFNQGLEBAENDICRYDVEVEDIS 120
 DB 61 NGVOSPRFPNSYPRLNLTWRLHSEONTRIQLVFNQGLEBAENDICRYDVEVEDIS 120
 QY 121 ESTTIIRGRWCGHKEVPRIKSRITNOIKITPKSDYFVAKPGFKIYYSLLDEFPQAAASE 180
 DB 121 ESTTIIRGRWCGHKEVPRIKSRITNOIKITPKSDYFVAKPGFKIYYSLLDEFPQAAASE 180
 QY 181 TNWESVTSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKTFNPESQEDLENNY 240
 DB 181 TNWESVTSISGVSYNSPSVTPTLLADALDKKIAEFDTVEDLLKTFNPESQEDLENNY 240
 QY 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVNIIRBELKLANVFFPRCLLVQ 300
 DB 241 LDTPRRGRSYHNRKSKVDRLNDADAKRYSCTPRPNYSVNIIRBELKLANVFFPRCLLVQ 300
 QY 301 RCGNGCGCTVWNRSCCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360
 DB 301 RCGNGCGCTVWNRSCCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIOLDHHERC 360

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Db      301  RCGNCGCGTVMNRSCNCSGKTVKHYEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy      361  DCICSSRRPR 370
Db      361  DCICSSRRPR 370

RESULT 18
ABP51640
ID      ABP51640 standard; protein, 370 AA.
XX
AC      ABP51640;
XX
DT      30-SEP-2002 (first entry)
XX
DE      Human zvegfg4 protein SEQ ID NO:2.
XX
KW      Human; zvegfg4; cell proliferation; extracellular matrix production;
KW      fibroproliferative disorder; PDGF-D; platelet derived growth factor;
KW      PDGF; vascular endothelial growth factor; VEGF; cytoskeletal; nephrotropic;
KW      hepatotropic; antiinflammatory; osteopathic; antiarthritic; metastasis;
KW      prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis;
KW      diabetic glomerulosclerosis; renal arteriosclerosis; nephrotic syndrome;
KW      chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis;
KW      hyperostosis; osteoarthritis.
XX
XX      Homo sapiens.
XX      OS
XX      US2002064832-A1.
XX
PD      30-MAY-2002.
XX
PF      14-MAR-2001; 2001US-00808972.
XX
PR      03-MAY-1999; 99US-0132250P.
PR      10-NOV-1999; 99US-0164463P.
PR      04-FEB-2000; 2000US-0180169P.
PR      03-MAY-2000; 2000US-0056459S.
PR      26-SEP-2000; 2000US-0235295P.
XX
PA      (HART/) HART C E.
PA      (TOPO/) TOPOUZIS S.
PA      (GILB/) GILBERTSON D G.
XX
PI      Hart CE, Topouzis S, Gilbertson DG;
XX
DR      WPI: 2002-573696/61.
DR      N-PSDB; AB073239.
XX
PT      Reducing proliferation of extracellular matrix production by a cell in a
PT      mammal, useful for treating fibroproliferative disorders of bone, liver
PT      and kidney, comprises administering a zvegfg4 antagonist.
XX
PS      Example 3; Page 19-20; 34p; English.
XX
CC      The present invention describes a method for reducing proliferation of or
CC      extracellular matrix production by a cell in a mammal. The method
CC      comprises administering to the mammal a composition comprising a
CC      zvegfg4 antibody, an inhibitory polynucleotide, inhibitors of zvegfg4
CC      activation, and mitogenically inactive, receptor-binding variants of
CC      zvegfg4. Zvegfg4 (also called PDGF-D) is a multi-domain protein that is
CC      structurally related to platelet derived growth factor (PDGF) and
CC      vascular endothelial growth factors (VEGF). Zvegfg4 has cytoskeletal,
CC      nephrotropic, hepatotropic, antiinflammatory, osteopathic and
CC      antiarthritic activities. The method is useful for reducing proliferation
CC      of mesangial, epithelial, endothelial, smooth muscle, fibroblast,
CC      osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells
CC      in a mammal, in particular proliferation of prostate tumour cells, and
CC      for reducing extracellular matrix production by a cell in a mammal
CC      suffering from a fibroproliferative disorder of kidney, bone or liver. In
CC      particular it is useful for reducing stellate cell activation. The method

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CC      is useful for reducing metastasis of prostate cancer cells to bone in a
CC      mammal and for treating a fibroproliferative disorder of kidney, liver or
CC      bone in a mammal. Fibroproliferative disorders of the kidney include,
CC      glomerulonephritis, diabetic glomerulosclerosis, lupus nephritis, renal
CC      arteriosclerosis and nephrotic syndrome, disorders of the liver include
CC      chronic active hepatitis and many other types of cirrhosis, and disorders
CC      of the bone include osteopetrosis, hyperostosis, osteosclerosis,
CC      osteoarthritis, and ectopic bone formation in metastatic prostate cancer.
CC      The present sequence represents human zvegfg4, which is used in an example
CC      from the present invention
XX
SQ      Sequence 370 AA;
XX
Query Match          100.0%; Score 370; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MRLIFVYTLICANFCSGRDTSATPQASIKALRNANLRDESNHLLDLYRRDPTIOVGK 60
Db      1  MRLIFVYTLICANFCSGRDTSATPQASIKALRNANLRDESNHLLDLYRRDPTIOVGK 60
Qy      61  NGVQSPRPFPNSYRNLLLTWRHLSQENTRIQLVFDNFGLEFANDICRYDFVEVDIS 120
Db      61  NGVQSPRPFPNSYRNLLLTWRHLSQENTRIQLVFDNFGLEFANDICRYDFVEVDIS 120
Qy      121  ESTIIRGRMGCHKEVPPIKSRITNOIKITFKSDDYFAKGGFKIYSLDFOPAAASE 180
Db      121  ESTIIRGRMGCHKEVPPIKSRITNOIKITFKSDDYFAKGGFKIYSLDFOPAAASE 180
Qy      181  TNWESVTSSISGSVNSPSTVPTLLADALDKIAEFDVBDLLKYFNPESQWEDLENMY 240
Db      181  TNWESVTSSISGSVNSPSTVPTLLADALDKIAEFDVBDLLKYFNPESQWEDLENMY 240
Qy      241  LDTPRYGRSYHDKRSKVDLRDLNDPAKRYSCTRPNYSVNIREFILANVVFPPCLLVQ 300
Db      241  LDTPRYGRSYHDKRSKVDLRDLNDPAKRYSCTRPNYSVNIREFILANVVFPPCLLVQ 300
Qy      301  RCGNCGCGTVMNRSCNCSGKTVKHYEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db      301  RCGNCGCGTVMNRSCNCSGKTVKHYEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy      361  DCICSSRRPR 370
Db      361  DCICSSRRPR 370

RESULT 19
ABU72430
ID      ABU72430 standard; protein, 370 AA.
XX
XX
AC      ABU72430;
XX
DT      17-JUN-2003 (first entry)
XX
DE      Human growth factor homologue ZVEGFA.
XX
KW      Human; growth factor homologue; ZVEGFA; proliferation; differentiation;
KW      migration; mesenchymal cell; cell surface semaphorin; neuropilin;
KW      neurite growth; cardiovascular development; limb development; cancer;
KW      cartilage development; T-cell; B-cell; Rheumatoid arthritis; cancer;
KW      autoimmune disease; inflammation; retinopathy; haemangioma;
KW      ischaemic event; neuropathy; acute nerve damage; stroke;
KW      central nervous system disease; peripheral nervous system disease;
KW      chromosome 11q22.3-23.1.
XX
OS      Homo sapiens.
XX
XX
FH      Key          Location/Qualifiers
FH      Region      52..370
FH      Region      /note= "Specifically claimed in claim 7"
FH      Region      52..253
FH      Region      /note= "Specifically claimed in claim 7"
FH      Region      180..370

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FT /note="Specifically claimed in claim 5"
FT 250..370
FT /note="Specifically claimed in claim 7"
FT 250..370
FT /note="Specifically claimed in claim 2"
FT 258..370
FT /note="Specifically claimed in claim 1"
XX US6495668-B1.
XX
XX 17-DEC-2002.
XX
XX 03-MAY-2000; 2000US-00564595.
XX
XX 03-MAY-1999; 99US-0132250P.
XX 10-NOV-1999; 99US-0164463P.
XX 04-FEB-2000; 2000US-0180169P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbert T, Hart CE, Shepard PO, Gilbertson DG;
XX WPI, 2003-352153/33.
XX N-PSDB; ACA64109.
XX
XX Isolated growth factor analogue ZVEGF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.
XX
XX Claim 1; Col 71-72; 67pp; English.
XX
XX The invention relates to an isolated protein comprising a first
CC polypeptide disulphide-bonded to a second polypeptide. The first and
CC second polypeptides are from 113-138 amino acid residues and comprises
CC 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
CC protein stimulates proliferation, differentiation, or migration of
CC mesenchymal cells and may modulate activities mediated by cell surface
CC semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
CC semaphorin interactions which may be of use in neurite growth,
CC cardiovascular development, cartilage and limb development, T- and B-cell
CC functions as well as treating rheumatoid arthritis, various forms of
CC cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas,
CC ischemic events, neuropathies, acute nerve damage, central nervous
CC system diseases and peripheral nervous system diseases including stroke.
CC The isolated protein is also used for a pharmaceutical composition as
CC therapeutic agents, diagnostic agents, and research tools and reagents.
CC It can be used in the study and regulation of cell and tissue
CC development, as components of cell culture media. The proteins can form
CC homooligomers or heterooligomers that act on tissues to control organ
CC development by modulating cell proliferation, migration, differentiation,
CC or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3
CC -23.1. The present sequence represents human ZVEGF4
XX
XX Sequence 370 AA:
XX
XX Query Match 100.0%; Score 370; DB 6; Length 370;
XX Best Local Similarity 100.0%; Pred. No.0;
XX Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRLRDESNHLLTDLYRDETTQVKS 60
XX 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRLRDESNHLLTDLYRDETTQVKS 60
XX
XX 61 NGVQSPRPFPNSYRNLLTLWRHLSQENTRIQVFNQSLBEAENDICRYDVEVEDIS 120
XX 61 NGVQSPRPFPNSYRNLLTLWRHLSQENTRIQVFNQSLBEAENDICRYDVEVEDIS 120
XX
XX 121 ETSITIRGRWCGKKEVPRIKSRITNOIKITFKSDVDVFAKPGFKIYYSLLEDDQPAASE 180
XX 121 ETSITIRGRWCGKKEVPRIKSRITNOIKITFKSDVDVFAKPGFKIYYSLLEDDQPAASE 180
XX
XX 181 TWMESVTSSISGVSYNSPVTDEPTLIADALDKKIAEDTVELLKYFNESMOEDLENNY 240
XX 181 TWMESVTSSISGVSYNSPVTDEPTLIADALDKKIAEDTVELLKYFNESMOEDLENNY 240
XX

Db 181 TWMESVTSSISGVSYNSPVTDEPTLIADALDKKIAEDTVELLKYFNESMOEDLENNY 240
Qy 241 LDPFRGRSSYHDRKSKVLDRLNDPAKRYSCPRPYSVINIRELLKLAUVFPPRLVVO 300
Db 241 LDPFRGRSSYHDRKSKVLDRLNDPAKRYSCPRPYSVINIRELLKLAUVFPPRLVVO 300
Qy 301 RCGNCGCGTVMWRSCCTCNSGKTVKKYHEVLOFEPGHIKRRGAKTMAVLDLDHHERC 360
Db 301 RCGNCGCGTVMWRSCCTCNSGKTVKKYHEVLOFEPGHIKRRGAKTMAVLDLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
XX
XX RESULT 20
XX ID ABG76397 standard; protein; 370 AA.
XX
XX ABG76397;
XX AC
XX DT 22-MAY-2003 (first entry)
XX
XX Human growth factor homologue, zvegf4.
XX
XX Human: growth factor homologue; zvegf4; fibroblast; smooth muscle cell;
KW cell-surface platelet-derived growth factor alpha receptor; PDGF;
KW full-thickness skin wound; female reproductive tract; duodenal ulcer;
KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;
KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;
KW chronic active hepatitis; hepatic chronic passive congestion; stroke;
KW central haemorrhagic necrosis; hepatic vein thrombosis; jaehaemia;
KW portal vein thrombosis; cardiac sclerosis; new vessel formation;
KW endothelial precursor stem cell; neovascularisation; wound healing;
KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;
KW sensory neurite outgrowth; brain damage; head injury; paralysis;
KW spinal injury; neurodegenerative disease; diabetic retinopathy;
KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;
KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;
KW proliferative vascular disorder; ocular neovascularisation;
KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;
KW angiogenesis; nervous system disorder; cytostatic; hepatocytic;
KW vulnary; tranquilliser; cerebroprotective; neuroprotective; nootropic;
KW ophthalmological; dermatological; coagulant; cardiant.
XX
XX OS Homo sapiens.
XX
XX US2002177193-A1.
XX
XX 28-NOV-2002.
XX
XX 02-MAY-2002; 2002US-00139583.
XX
XX 07-DEC-1998; 98US-011173P.
XX 06-JUL-1999; 99US-0142576P.
XX 21-OCT-1999; 99US-0161653P.
XX 12-NOV-1999; 99US-0165255P.
XX 07-DEC-1999; 99US-00457066.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gao Z, Hart CE, Piddington CS, Shepard PO, Shoemaker KE;
XX Gilbertson DG, West JW;
XX WPI, 2003-328465/31.
XX N-PSDB; ABX93177.
XX
XX New isolated zvegf3 polypeptide, useful for treating cancer, Alzheimer's
PT disease, Parkinson's disease, chronic active hepatitis, hepatic vein
PT thrombosis, comprises growth factor domain and CUB domain.
XX
XX Disclosure; Page 51-52; 73pp; English.
XX

CC The present invention relates to the isolation of a growth factor
CC homologue referred to as zvegf3, and the polynucleotide sequence encoding
CC it. The zvegf3 polypeptide is useful for stimulating the growth of
CC fibroblasts or smooth muscle cells, or for activating a cell-surface
CC platelet-derived growth factor (PDGF) alpha receptor. The zvegf3
CC polypeptide is useful as a PDGF alpha receptor agonist and thus is useful
CC for treating full-thickness skin wounds, female reproductive tract and
CC prolonged bleeding, periodontal disease, damaged liver tissue, and
CC duodenal ulcers. The polypeptide is also useful as an additive in tissue
CC adhesives for promoting revascularisation of healing tissue. The zvegf3
CC polypeptide is also useful for treating liver damage including damage due
CC to liver disease, chronic active hepatitis, hepatic chronic passive
CC congestion (CCP), central haemorrhagic necrosis (CHN), hepatic vein
CC thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of
CC cirrhosis. The polypeptide is useful for enhancing expansion and
CC stabilisation of endothelial precursor stem cells, creating and
CC stabilising new vessel formation in areas requiring neovascularisation,
CC including areas of ischemia, organ transplants, wound healing, and
CC tissue grafting. It may be used for treating peripheral neuropathies by
CC increasing spinal cord and sensory neurite outgrowth, and as part of
CC therapeutic treatment for the regeneration of neurite outgrowths
CC following strokes, brain damage caused by head injuries, and paralysis
CC caused by spinal injuries. Application may also be made in treating
CC neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease), diabetic retinopathy, psoriasis, arthritis,
CC scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung
CC fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds
CC zvegf3 is useful for blocking the mitogenic, chemocactic, or angiogenic
CC effects of zvegf3, and for treating proliferative vascular disorders,
CC ocular neovascularisation, inflammatory disorders, rheumatoid arthritis,
CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,
CC and diseases of the nervous system. The present sequence represents human
CC zvegf4
CC
XX

SQ Sequence 370 AA:

Query Match 100.0%; Score 370; DB 6; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLFFVTLICANCSGCDTATPOSASIKALRNANLRDSSNHLTDLYRDETIQVKG 60
DB 1 MHRLFFVTLICANCSGCDTATPOSASIKALRNANLRDSSNHLTDLYRDETIQVKG 60
QY 61 NGYVSPRPFPNSYPENLLTWRLHSQENTRIQLVFNQGLSEANDICRYFVEVDIS 120
DB 61 NGYVSPRPFPNSYPENLLTWRLHSQENTRIQLVFNQGLSEANDICRYFVEVDIS 120
QY 121 ESTTIRGRWCGHKEVPPIKRTNQIKITFKSDYFVAKPGFKIYSLIEDPQPAASE 180
DB 121 ESTTIRGRWCGHKEVPPIKRTNQIKITFKSDYFVAKPGFKIYSLIEDPQPAASE 180
QY 121 ESTTIRGRWCGHKEVPPIKRTNQIKITFKSDYFVAKPGFKIYSLIEDPQPAASE 180
DB 121 ESTTIRGRWCGHKEVPPIKRTNQIKITFKSDYFVAKPGFKIYSLIEDPQPAASE 180
QY 121 TWNEVTSISGSVNSPSVNDPTLLADLDKKIEFPDVEELLKYFNPESQOELENNY 240
DB 121 TWNEVTSISGSVNSPSVNDPTLLADLDKKIEFPDVEELLKYFNPESQOELENNY 240
QY 121 TWNEVTSISGSVNSPSVNDPTLLADLDKKIEFPDVEELLKYFNPESQOELENNY 240
DB 121 TWNEVTSISGSVNSPSVNDPTLLADLDKKIEFPDVEELLKYFNPESQOELENNY 240
QY 241 LDTPEYRGRSYHDRSKYVDLRLNDADAKYSCTPPNYSVNIIEEKLNAVVFPPCLLVQ 300
DB 241 LDTPEYRGRSYHDRSKYVDLRLNDADAKYSCTPPNYSVNIIEEKLNAVVFPPCLLVQ 300
QY 241 LDTPEYRGRSYHDRSKYVDLRLNDADAKYSCTPPNYSVNIIEEKLNAVVFPPCLLVQ 300
DB 241 LDTPEYRGRSYHDRSKYVDLRLNDADAKYSCTPPNYSVNIIEEKLNAVVFPPCLLVQ 300
QY 301 RCGNCGCGCTVNMRSCTCNSGKTVKKYHEVLQPEFGHKKRGRAKTMAVLVDLHDHHERC 360
DB 301 RCGNCGCGCTVNMRSCTCNSGKTVKKYHEVLQPEFGHKKRGRAKTMAVLVDLHDHHERC 360
QY 361 DCICSSRPFR 370
DB 361 DCICSSRPFR 370

RESULT 21
ABB80134
ID ABB80134 standard; protein; 370 AA.
XX

AC ABB80134;
XX
DT 27-JUN-2003 (first entry)
XX
DE PDGF-D.
XX
XX Nervous system; platelet-derived growth factor; PDGF; psychosis;
KW Vascular endothelial growth factor; VEGF; neural; stem cell; mucoly;
KW progenitor cell; neurodegeneration; ischemia; neurological trauma;
KW neuropsychiatry; learning; Parkinson's disease; Huntington's disease;
KW Amyotrophic lateral Sclerosis; spinal ischemia; ischemic stroke;
KW spinal cord injury; cancer-related; schizophrenia; Alzheimer's disease;
KW depression; anxiety; phobia; stress; cognitive function; aggression;
KW drug; alcohol; abuse; obsessive compulsive behaviour; proliferation;
KW seasonal mood disorder; personality disorder; cerebral palsy;
KW multi-infarct; dementia; Lewy body; age related; geriatric; growth;
KW epilepsy; brain injury; multiple sclerosis; autism; differentiation;
KW attention deficit disorder; narcolepsy.
XX
OS Homo sapiens.
XX
PN WO2003024478-A1.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-1B003998.
XX
PR 19-SEP-2001; 2001US-0323381P.
XX
PR 28-SEP-2001; 2001US-0326044P.
XX
PA (NEUR-) NEURONOVA AB.
XX
PI Delfant K, Janson AM, Kuhn GH, Plate K, Schanzer A, Wachs F;
PI Zhao M;
XX
XX WPI: 2003-354563/33.
XX
DR N-PSDB; ABQ80246.
XX
PT Use of platelet-derived growth factor, vascular endothelial growth
PT factor, or their modulators for modulating neural stem cell or neural
PT progenitor cell activity, particularly for treating e.g. Alzheimer's,
PT ischemia or stroke.
XX
PS Disclosure; Page 23; 119pp; English.
XX
XX The sequences given in ABB80131-35 show proteins which may be used in the
XX method of the invention for alleviating or reducing a symptom of a
XX disease or disorder of the nervous system. The method comprises
XX administering platelet-derived growth factor (PDGF), vascular endothelial
XX growth factor (VEGF), a combination of PDGF and VEGF, or a PDGF or VEGF
XX agonist, to a patient in order to modulate neural stem cell or neural
XX progenitor cell activity in vivo. The method is useful for alleviating or
XX reducing the symptoms of a disease or disorder of the nervous system,
XX e.g. neurodegenerative disorders, neural stem cell disorders, neural
XX progenitor disorders, ischemic disorders, neurological traumas,
XX affective disorders, neuropsychiatric disorders or learning and memory
XX disorders. In particular, the method is useful for alleviating or
XX treating Parkinson's disease and disorders, Huntington's disease,
XX Alzheimer's disease, Amyotrophic lateral Sclerosis, spinal ischemia,
XX ischemic stroke, spinal cord injury or cancer-related brain/ spinal cord
XX injury, schizophrenia and other psychoses, depression, bipolar
XX depression/disorder, anxiety syndromes/disorders, phobias, stress and
XX related syndromes, cognitive function disorders, aggression, drug and
XX alcohol abuse, obsessive compulsive behaviour syndromes, seasonal mood
XX disorder, borderline personality disorder, cerebral palsy, life style
XX drug, multi-infarct dementia, Lewy body dementia, age related/geriatric
XX dementia, epilepsy and injury related to epilepsy, spinal cord injury,
XX brain injury, trauma related brain/spinal cord injury, infection and
XX treatment related brain/spinal cord tissue injury, infection and
XX inflammation related brain/spinal cord injury, environmental toxin
XX related brain/spinal cord injury, multiple sclerosis, autism, attention
XX deficit disorders, narcolepsy or sleep disorders. The PDGF and/or VEGF,
XX is useful in the manufacture of a medicament for alleviating or treating

CC these diseases or disorders, accelerating growth of neural stem cells or
CC neural progenitor cells, or inducing proliferation or differentiation of
CC these cells

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
DB 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
QY 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEPQPAASE 180
DB 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEPQPAASE 180
QY 181 TNWESYTSSISGVSYNSPSVTPTLADALDKKIAEFVIEDLLKTFNPESMOEDLENNY 240
DB 181 TNWESYTSSISGVSYNSPSVTPTLADALDKKIAEFVIEDLLKTFNPESMOEDLENNY 240
QY 241 LDTPRYGRSYPHRSKVDLRLNDADAKRYSCTPRPNYSVINIRELKLAVVFFPRCLLVQ 300
DB 241 LDTPRYGRSYPHRSKVDLRLNDADAKRYSCTPRPNYSVINIRELKLAVVFFPRCLLVQ 300
QY 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVDIOLDHHERC 360
DB 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 22

ABR43944
ID ABR43944 standard; protein; 370 AA.

XX AC ABR43944;

XX DT 11-AUG-2003 (first entry)

XX DE Human PDGF-D polypeptide.

XX KW Platelet-derived growth factor-D; PDGF-D; osteopathic; vulnary; bone;
XX connective tissue; human.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

FT Domain 258..365
FT /note="core growth factor domain"

XX PN WO2003033677-A2.

XX PD 24-APR-2003.

XX PF 18-OCT-2002; 2002WO-US033563.

XX PR 19-OCT-2001; 2001US-0346117P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Moore MD, Fox BA;

XX DR WPI; 2003-421322/39.

XX DR N-PSDB; ACC47941.

PT New protein consisting of two platelet-derived growth factor-D
PT polypeptide chains, useful for stimulating the production of bone and/or
PT connective tissue in both humans and animals, e.g. in treating fractures
PT or osteoporosis.

XX PS Claim 1; Page 34-37; 47pp; English.

XX CC The invention relates to a protein consisting of two platelet-derived
XX growth factor-D (PDGF-D) polypeptide chains. The protein is useful in
XX enhanced production of PDGF-D growth factor domain dimers. It may be used
XX to stimulate production of bone and/or connective tissue in both humans
XX and animals, such as in cases of fractures, bone grafts, implants, repair
XX of bony defects arising from surgery, surgical reconstruction following
XX traumatic injury, repair of hereditary or other physical abnormalities,
XX or in treatment of osteoporosis. The present sequence represents a human
XX PDGF-D polypeptide

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
DB 1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
QY 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPRPFPNSYPRLNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
QY 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEPQPAASE 180
DB 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEPQPAASE 180
QY 181 TNWESYTSSISGVSYNSPSVTPTLADALDKKIAEFVIEDLLKTFNPESMOEDLENNY 240
DB 181 TNWESYTSSISGVSYNSPSVTPTLADALDKKIAEFVIEDLLKTFNPESMOEDLENNY 240
QY 241 LDTPRYGRSYPHRSKVDLRLNDADAKRYSCTPRPNYSVINIRELKLAVVFFPRCLLVQ 300
DB 241 LDTPRYGRSYPHRSKVDLRLNDADAKRYSCTPRPNYSVINIRELKLAVVFFPRCLLVQ 300
QY 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVDIOLDHHERC 360
DB 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 23

AAE38476
ID AAE38476 standard; protein; 370 AA.

XX AC AAE38476;

XX DT 20-NOV-2003 (first entry)

XX DE Human platelet derived growth factor (PDGF-D).

XX KW Human; platelet-derived growth factor-D; PDGF-D; bone graft; osteopathic;
XX radiation-induced osteonecrosis; periodontal disease; protein therapy;
XX joint injury; osteoporosis; bone loss; fracture; bone healing.

XX OS Homo sapiens.

XX FT Key

FT Region 1..18
FT /note="Secretory peptide"

FT Domain 52..179

FT /note="CUB domain"

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENHNTDLYRRDETIOVNG 60
 DB 1 MHRLLFVYTLICANFCSCRDTSATPOSASIKALRNANLRDSENHNTDLYRRDETIOVNG 60

QY 61 NGYVSPRPNSYPNNLLTWRLHSQENTRIQLVFQNGGLEBAENDICRYDFVEVEDIS 120
 DB 61 NGYVSPRPNSYPNNLLTWRLHSQENTRIQLVFQNGGLEBAENDICRYDFVEVEDIS 120

QY 121 EFTSTIIRGWCCHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYSLLEDPQPAASE 180
 DB 121 EFTSTIIRGWCCHKEVPPRIKSRNQIKITPKSDDYFVAKPGFKIYSLLEDPQPAASE 180

QY 181 TWMESTYSISGVSYNSPSVTPDTLLADALDKKIAEFDVEDLLKYNFESWQEDLENNY 240
 DB 181 TWMESTYSISGVSYNSPSVTPDTLLADALDKKIAEFDVEDLLKYNFESWQEDLENNY 240

QY 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300
 DB 241 LDTPRYGRSYHDRKSKVDLRLNDADAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQ 300

QY 301 RCGNGCGCTVNMRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
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 AC ADG47746;
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 DT 11-MAR-2004 (first entry)
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 DE Human zvegfg3 related protein.
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 KW Vulnerary; dermatological; wound healing; proliferation; zvegfg3.; human.
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 OS Homo sapiens.
 XX
 PN US6528050-B1.
 XX
 PD 04-MAR-2003.
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 PF 06-NOV-2000; 2000US-00706968.
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 PR 07-DEC-1998; 98US-0111173P.
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 PR 21-OCT-1999; 99US-0161653P.
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 PR 07-DEC-1999; 99US-00457066.
 PR 31-MAR-2000; 2000US-00541752.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gao Z, Hart CE, Piddington CS, Shepard PO, Shoemaker KB;
 PI Gilbertson DG, West JW;
 XX
 DR WPI; 2003-370630/35.
 DR N-PSDB; ADG47745.
 XX
 PT Promoting wound healing or proliferation of fibroblasts or smooth muscle
 PT cells in a mammal, by administering a polypeptide comprising growth
 PT factor domain of human growth factor homolog polypeptide, zvegfg3.
 PS Disclosure; SEQ ID NO 37; 69pp; English.
 CC The present invention relates to a method of promoting wound healing,

CC especially a dermal wound and for promoting proliferation of fibroblasts
 CC or smooth muscle cells in a mammal, by administering a polypeptide
 CC comprising growth factor domain of human growth factor homolog
 CC polypeptide, zvegfg3. The present sequence is human zvegfg3 related
 CC protein.

SQ Sequence 370 AA;

Query Match 100.0%; Score 370; DB 7; Length 370;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 DCICSSRPPR 370
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 Job time : 167 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:37:22 : Search time 43 Seconds
(without alignments)
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Perfect score: 370
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Searched: 513545 seqs, 74649064 residues

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Total number of hits satisfying chosen parameters: 14506

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	370	100.0	370	4	US-09-540-224-2
3	370	100.0	370	4	US-09-564-595D-2
4	370	100.0	370	4	US-09-706-968-37
5	370	100.0	370	4	US-09-808-972-2
6	370	100.0	370	4	US-09-823-033-5
7	370	100.0	370	4	US-09-438-046-8
8	370	100.0	370	4	US-10-139-583-37
9	370	100.0	370	4	US-10-039-847A-2
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ALIGNMENTS

RESULT 1

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; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
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; ORGANISM: Homo sapiens
US-09-457-066-37
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; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
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; Patent No. 6493668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
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QY 361 DCICSSRPPR 370
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/ Patent No. 6528050
/ GENERAL INFORMATION:
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Gao, Zeren
/ APPLICANT: Piddington, Christopher S.
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Shoemaker, Kimberly E.
/ APPLICANT: Gilbertson, Debra G.
/ APPLICANT: West, James W.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
/ FILE REFERENCE: 98-60C1
/ CURRENT APPLICATION NUMBER: US/09/706, 968
/ CURRENT FILING DATE: 2000-11-06
/ PRIOR APPLICATION NUMBER: US/09/541,752
/ PRIOR FILING DATE: 2000-03-31
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 37
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-706-968-37

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Best Local Similarity 100.0%; Pred. No. 0;
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QY 361 DCICSSRPPR 370
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Db 361 DCICSSRPPR 370
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RESULT 5

US-09-808-972-2
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/ Patent No. 6630142
/ GENERAL INFORMATION:
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Topouzis, Stavros
/ APPLICANT: Gilbertson, Debra G.
/ TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
/ FILE REFERENCE: 00-79
/ CURRENT APPLICATION NUMBER: US/09/808, 972
/ CURRENT FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: US 60/235, 295
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/564, 595
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 60/180, 169
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/164, 463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/132, 250
/ PRIOR FILING DATE: 1999-05-03
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-808-972-2

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHRLIFVYTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
Db 1 MHRLIFVYTLICANFSCCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRDETTQVKG 60
| | | | |
QY 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
Db 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQFGLBEAENDICRYDVEVEDIS 120
| | | | |
QY 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDPQPAASE 180
| | | | |
Db 121 ETSIIIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDPQPAASE 180
| | | | |
QY 181 TNWESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |
Db 181 TNWESVTSSISGVSYNSPSVTPTLLADALDKKIAEFDVIEDLLKYNPESWQEDLENNY 240
| | | | |
QY 241 LDTPRYRGRSYHDKRSKVDLDRLNDPAKRYSCPTPRNYSVINIREELKLANVFFPRCLLVQ 300
| | | | |
Db 241 LDTPRYRGRSYHDKRSKVDLDRLNDPAKRYSCPTPRNYSVINIREELKLANVFFPRCLLVQ 300
| | | | |
QY 301 RCGNGCGCTVNMRSCTCNSGKTVMKKYHEVLOEPGHIKRRGAKTMALVDIQLDHHERC 360
| | | | |

Db	301	RCGGNCGCGTAAWRSTCGNSGKTVKKYHEVLFEFGHILKRGRAKTAALVLDIDHHNRC	360
Qy	361	DCICSSRPPR	370
Db	361	DCICSSRPPR	370

RESULT 6
US-09-823-033-5
; Sequence 5, Application US/09823033

```

: GENERAL INFORMATION:
: APPLICANT: Hart, Charles E.
: TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE
: TITLE OF INVENTION: LIGAMENT AND CARTILAGE
: FILE REFERENCE: 00-12
: CURRENT APPLICATION NUMBER: US/09/823,033
: CURRENT FILING DATE: 2001-03-29
: NUMBER OF SEQ. ID NOS.: 5
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ. ID NOS.:

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Query March	370;	Score	370;	DB	4;	Length	370;
Best Local	Similarly	100.0%;	Pred. No.	0;			
Matches	370;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

[illegible]

Db 121 ETSIIIRGNCGHKEVPPRIKSRITQIKITFKSDYFVAKGFKIYSLLEDFQPAASE 180

Db	181	TNME\$VTSSISGV\$YNSP\$VTDPTULADADKIAEFDTYVEDLLKXFNPE\$MQEDELNMY	240
Oy	241	LDTPRYRG\$SYHDK\$K\$VDLDR\$LANDAKR\$V\$CTPRNY\$VNI\$REEL\$KIANV\$VFPRCLL\$VQ	300

QY 301 RCGNGCGGTVMNRSTCNSGKTVKKYHEVLQEPCHIKRGRAKTMALVDIQLDHHRC 360

Qy 361 DCICSSRPPR 370
 |||||
b 361 DCICSSRPPR 370

RESULT 7
US-09-438-046-8

US-09-438-046-8
Sequence 8, Application US/09438046
Parent No. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: ABE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTN, Monica
APPLICANT: UTEHL, Mario
APPLICANT: ALTHAN, Karl
APPLICANT: OSTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik

```

; TITLE OF INVENTION: PLATELET-DERIVED GROWTHFACTOR D, DNA CODING
;
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
;
; FILE REFERENCE: Ulf Eriksson et al 1064-44033
;
; CURRENT APPLICATION NUMBER: US/09/438,046

```

EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/113,993
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,600
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,755
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31

Query Match	100.0%	Score 370;	DB 4;	Length 370;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 370; Conservative	0;	Mismatches	0;	Gaps 0;

Dy 61 NGVQSRPFNSYPRLNLLTWRLHSQENRIQLVFDNQGEEANDICRYDFVEVEDIS 120
 |||||
Dz 61 NGVQSRPFNSYPRLNLLTWRLHSQENRIQLVFDNQGEEANDICRYDFVEVEDIS 120
 |||||

121 EISTTIGRWCGHKEVPPRIKSRNTQIKITFKSDDYFAKPGFKIYSSLEDFQPAASE 180

Db 181 INWESVTSSISGVSYNSPSTDTPLTADALDKIAEFDYVEDLLKYFNPSWQEDDENMY 240

Oy 241 LDTPRYRGRSYHDKSKVDLRLNDADAKRYSCPTPRNYSVNIREFKLAVVFFPRCLLVQ 300

301 RCGGCGCGTVMRSTCNSGKTVKKYHEVLQEPGHIRRGRAKTALVDIQDHERC 360

DY 361 DCICSSRPPR 370
 |||||
hb 361 DCTCSSRPPR 370

RESULT 8
US-10-139-583-37
Sequence 37 Amplification: 16/10100000

RESULT 8
 US-10-139-583-37
 ; Sequence 37, Application US/10139583
 Patent No. 6814965
 GENERAL INFORMATION:
 APPLICANT: Gao, Zeren
 APPLICANT: Hart, Charles E.
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Shoemaker, Kimberly E.
 APPLICANT: Gilbertson, Debora G.
 APPLICANT: West, James W.
 TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
 FILE REFERENCE: 98-60
 CURRENT APPLICATION NUMBER: US/10/139,583
 CURRENT FILING DATE: 2002-05-02
 PRIOR APPLICATION NUMBER: 09/457,066

PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37
LENGTH: 370
TYPE: PR1
ORGANISM: Homo sapiens
US-10-139-583-37

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
DB 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
QY 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFDNQGLEBAENDICRYDVEVEDIS 120
DB 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFDNQGLEBAENDICRYDVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYSSLEDFOPAAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYSSLEDFOPAAASE 180
QY 181 TMNESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKFNPSWQEDLENMY 240
DB 181 TMNESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKFNPSWQEDLENMY 240
QY 241 LDTPRYGRS YHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVFFPRCLVQ 300
DB 241 LDTPRYGRS YHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVFFPRCLVQ 300
QY 301 RCGNGCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHGIRKGRAKTALVDIOLDHHERC 360
DB 301 RCGNGCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHGIRKGRAKTALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 9

US-10-039-847A-2
Sequence 2, Application US/10039847A
Patent No. 6827938
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
FILE REFERENCE: 00-100
CURRENT APPLICATION NUMBER: US/10/039,847A
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/244,479
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PR1
ORGANISM: Homo sapiens
US-10-039-847A-2

Query Match 100.0%; Score 370; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
DB 1 MRLIFVYTLICANFSCRDTSATPOSASIKALRNANLRDESNHLLTDLYRRETTIOVKG 60
QY 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFDNQGLEBAENDICRYDVEVEDIS 120

DB 61 NGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFDNQGLEBAENDICRYDVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYSSLEDFOPAAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYSSLEDFOPAAASE 180
QY 181 TMNESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKFNPSWQEDLENMY 240
DB 181 TMNESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKFNPSWQEDLENMY 240
QY 241 LDTPRYGRS YHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVFFPRCLVQ 300
DB 241 LDTPRYGRS YHDKRSKVDLRLNDADAKRYSCTPRNYSVNI REELKLANVFFPRCLVQ 300
QY 301 RCGNGCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHGIRKGRAKTALVDIOLDHHERC 360
DB 301 RCGNGCGCGTVMNRSTCNSGKTVKKYHEVLOPEPHGIRKGRAKTALVDIOLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 10

US-09-438-046-6
Sequence 6, Application US/09438046
Patent No. 670687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: IEE, Xuri
APPLICANT: PORTN, Annica
APPLICANT: UTELLA, Marco
APPLICANT: ALTALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 322
TYPE: PR1
ORGANISM: Homo sapiens
US-09-438-046-6

Query Match 87.0%; Score 322; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2,5e-305;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 LYRRETTIOVKGNGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFDNQGLEBAENDI 108
DB 1 LYRRETTIOVKGNGVQSPRFPNSYPRNLLTWRLHSGENTRIQLVFDNQGLEBAENDI 108
QY 109 CRYDVEVEDISSTIIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYSS 168
DB 61 CRYDVEVEDISSTIIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKPGFKIYSS 120
QY 169 LLEDFOPAASETNMESVTSSISGVSYNSPSVTDPTLADALDKKIAEFDVIEDLLKYN 228

```
Db 121 LLEDFOPAASSTWESYSSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKYPN 180
Qy 229 PESWEDLENNYLDTPRYGRGRSYHDKRSVVDLDRINDDAKRSCPTPRNYSVNIIBELKLA 288
Db 181 PESWEDLENNYLDTPRYGRGRSYHDKRSVVDLDRINDDAKRSCPTPRNYSVNIIBELKLA 240
Qy 289 NVFFPRCLLVORCGGCGTVMNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA 348
Db 241 NVFFPRCLLVORCGGCGTVMNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA 300
Qy 349 LVDIOLDHHERCDCICSSRPPR 370
Db 301 LVDIOLDHHERCDCICSSRPPR 322

RESULT 11
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; ORGANISM: Artificial Sequence
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGPA4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match 55.9%; Score 207; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-193; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 RDETIQVKGNGYVQSPREFNSYPRNLLTWRLHSEENTRIQLVFDNQGLEBAENDICRY 111
Db 1 RDETIQVKGNGYVQSPREFNSYPRNLLTWRLHSEENTRIQLVFDNQGLEBAENDICRY 60
Qy 112 DFEVEDISESTIIRGRWCGHKEVPPRKSTNTQIKITFKSDDYFVAKPGFKIYSLLE 171
Db 61 DFEVEDISESTIIRGRWCGHKEVPPRKSTNTQIKITFKSDDYFVAKPGFKIYSLLE 120
Qy 172 DFOPAASSTWESYSSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKYPN 231
Db 121 DFOPAASSTWESYSSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKYPN 180
Qy 232 WOEDLENNYLDTPRYGRGRSYHDKRSKV 258
Db 181 WOEDLENNYLDTPRYGRGRSYHDKRSKV 207

RESULT 12
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; ORGANISM: Artificial Sequence
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
```

```
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGPA4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match 51.6%; Score 191; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 9.5e-178; Indels 0; Gaps 0;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 ETNNESTYSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKYPNPSWEDLENN 239
Db 126 ETNNESTYSISGVSYNSPSVTDPTLLADALDKKIAEDTVEDLLKYPNPSWEDLENN 185
Qy 240 YLDPTRYGRGRSYHDKRSVVDLDRINDDAKRSCPTPRNYSVNIIBELKLA;NVFFPRCLLV 229
Db 186 YLDPTRYGRGRSYHDKRSVVDLDRINDDAKRSCPTPRNYSVNIIBELKLANVFFPRCLLV 245
Qy 300 QRCGNGCGTVMNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA;LVDIOLDHHER 359
Db 246 QRCGNGCGTVMNRSCCTNSGKTVKKYHEVLOJEPGHIKRGRAKTMA;LVDIOLDHHER 305
Qy 360 CDCICSSRPPR 370
Db 306 CDCICSSRPPR 316

RESULT 13
US-09-564-595D-57
; Sequence 57, Application US/09564595D
; Patent No. 6495668
; ORGANISM: Artificial Sequence
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGPA4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

Query Match 34.6%; Score 128; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 2.1e-116; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      52  RDETTQVGNCGVQSPRPNSVPRNLLTWTWRHSGENRIQLVFPNPGLEAENDICRY 111
Db      1  RDETTQVGNCGVQSPRPNSVPRNLLTWTWRHSGENRIQLVFPNPGLEAENDICRY 60

Qy      112 DFEVEDISESTTIIRGRWCGHKEVPPRIKSRTNOIKITFKSDDYFVAKPGFKIYSLLE 171
Db      61  DFEVEDISESTTIIRGRWCGHKEVPPRIKSRTNOIKITFKSDDYFVAKPGFKIYSLLE 120

Qy      172 DFQPAAS 179
Db      121 DFQPAAS 128

RESULT 14
US-09-438-046-19
; Sequence 19, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: ALITALO, Marko
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-19

Query Match      32.2%; Score 119; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 5.5e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      52  RDETTQVGNCGVQSPRPNSVPRNLLTWTWRHSGENRIQLVFPNPGLEAENDICRY 111
Db      1  RDETTQVGNCGVQSPRPNSVPRNLLTWTWRHSGENRIQLVFPNPGLEAENDICRY 60

Qy      112 DFEVEDISESTTIIRGRWCGHKEVPPRIKSRTNOIKITFKSDDYFVAKPGFKIYSLLE 170
Db      61  DFEVEDISESTTIIRGRWCGHKEVPPRIKSRTNOIKITFKSDDYFVAKPGFKIYSLLE 119

RESULT 15
US-09-438-046-4
; Sequence 4, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: TUTELA, Marko
; APPLICANT: ALITALO, Kari

```

```
Qy 318 CNSGTVKYYHEVLOFEPGHIKRRGRATMALVDIQLDHERCDICSSRPPR 370
Db 250 CNSGTVKYYHEVLOFEPGHIKRRGRATMALVDIQLDHERCDICSSRPPR 302

RESULT 17
US-09-438-046-2
; Sequence 2, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: TUTELA, Mariko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-438-046-2

Query Match 17.8%; Score 66; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 NCGCTVWVRSTCTNSGTVKYYHEVLOFEPGHIKRRGRATMALVDIQLDHERCDIC 364
Db 1 NCGCTVWVRSTCTNSGTVKYYHEVLOFEPGHIKRRGRATMALVDIQLDHERCDIC 60

Qy 365 SSRPPR 370
Db 61 SSRPPR 66

RESULT 18
US-09-438-046-18
; Sequence 18, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: TUTELA, Mariko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
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/ EARLIER APPLICATION NUMBER: 60/107,852
/ EARLIER FILING DATE: 1998-11-10
/ EARLIER APPLICATION NUMBER: 60/113,997
/ EARLIER FILING DATE: 1999-12-28
/ EARLIER APPLICATION NUMBER: 60/150,604
/ EARLIER FILING DATE: 1999-08-26
/ EARLIER APPLICATION NUMBER: 60/157,108
/ EARLIER FILING DATE: 1999-10-04
/ EARLIER APPLICATION NUMBER: 60/157,756
/ EARLIER FILING DATE: 1999-10-05
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 18
/ TYPE: PRT
/ LENGTH: 121
/ ORGANISM: Homo sapiens
US-09-438-046-18

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Db 1 SYHDKSKVDDRLNDDAKRYSCTPRNYSVNIREELKANVFPFRCLLVORCGNCGG 60

Qy 310 TV 311
Db 61 TV 62

RESULT 19
US-09-540-224-4
; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZV6GF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4

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Best Local Similarity 100.0%; Pred. No. 5.8e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 SRTNOKITFKSDDYFVAKPGFKIYYS 168
Db 142 SRTNOKITFKSDDYFVAKPGFKIYYS 168

RESULT 20
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; Sequence 53, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZV6GF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
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; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-564-595D-53
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Best Local Similarity 100.0%; Pred.No. 5.8e-18;
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; Sequence 4, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-808-972-4
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Best Local Similarity 100.0%; Pred.No. 5.8e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 4, Application US/10039847A
; Patent No. 6827938
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
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; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
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; ORGANISM: Mus musculus
US-10-039-847A-4
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; Sequence 8, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGFA
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-540-224-8
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US-09-564-595D-40
; Sequence 40, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGFA
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
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; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide
 US-09-564-595D-40

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 Best Local Similarity 100.0%; Pred. No. 4.9e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ESMQEDLENMYLDTPRYRGRSYHD 24

RESULT 25
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 ; Sequence 10; Application US/09808972
 ; Patent No. 6630142
 ; GENERAL INFORMATION:
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Topouzis, Stavros
 ; APPLICANT: Gilbertson, Debra G.
 ; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
 ; FILE OF INVENTION: DISORDERS
 ; FILE REFERENCE: 00-79
 ; CURRENT APPLICATION NUMBER: US/09/808,972
 ; CURRENT FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: US 60/235,295
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US 09/564,595
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 60/180,169
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/164,463
 ; PRIOR FILING DATE: 1999-11-10
 ; PRIOR APPLICATION NUMBER: US 60/132,250
 ; PRIOR FILING DATE: 1999-05-03
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide
 US-09-808-972-10

Query Match 6.5%; Score 24; DB 4; Length 25;
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 Db 1 ESMQEDLENMYLDTPRYRGRSYHD 24

Search completed: November 10, 2005, 09:48:22
 Job time : 44 secs

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OM protein - protein search, using sw model

Run on: November 10, 2005, 09:41:13 : Search time 165 Seconds
(without alignments)
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Title: US-10-606-055-2

Perfect score: 370

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Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	370	100.0	370	9	US-09-915-582-56
4	370	100.0	370	11	US-09-876-813-2
5	370	100.0	370	11	US-09-833-245-1482
6	370	100.0	370	13	US-10-086-623-8
7	370	100.0	370	13	US-10-039-583-37
8	370	100.0	370	13	US-10-039-847A-2
9	370	100.0	370	14	US-10-260-539-8
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13	370	100.0	370	14	US-10-274-638-2	Sequence 2, Appl1
14	370	100.0	370	14	US-10-011-364-4	Sequence 4, Appl1
15	370	100.0	370	14	US-10-277-862-56	Sequence 56, Appl1
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19	370	100.0	370	15	US-10-606-055-2	Sequence 2, Appl1
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31	370	100.0	370	20	US-11-021-088-37	Sequence 37, Appl1
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ALIGNMENTS

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RESULT 1
US-09-823-033-5
; Sequence 5, Application US/09823033
; Patent No. US2002004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-5
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Query Match 100.0%; Score 370; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKGPFKIYSLLEDFQPAASE 180
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RESULT 2
US-09-808-972-2
; Sequence 2, Application US/09808972
; Patent No. US20020064832A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROBLASTIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/735,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-972-2
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Query Match 100.0%; Score 370; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
DB 1 MHRLIFVYTLICANFCSCRDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
QY 61 NGVQSPFPNSYPNNLLTWRHLSQENTRIQLVFDNQFGLEAENDICRYDFVEVEDIS 120
DB 61 NGVQSPFPNSYPNNLLTWRHLSQENTRIQLVFDNQFGLEAENDICRYDFVEVEDIS 120
QY 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKGPFKIYSLLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITPKSDDYFVAKGPFKIYSLLEDFQPAASE 180
QY 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVBDLLKYFNPESQOEDLEMY 240
DB 181 TNWESVTSISGVSNPSVTDPTLIADALDKKIAEFTVBDLLKYFNPESQOEDLEMY 240
QY 241 LDTPRYRGRSYHDRKSKVDLDRNDADAKRYSCTRPNYSVNI REBELKLANVVFPPCLLVQ 300
DB 241 LDTPRYRGRSYHDRKSKVDLDRNDADAKRYSCTRPNYSVNI REBELKLANVVFPPCLLVQ 300
QY 301 RCGNGCGGTVMNSCTCNSGKTVKHYEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNGCGGTVMNSCTCNSGKTVKHYEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370
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RESULT 3
US-09-915-582-56
; Sequence 56, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: P5723b1
```

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; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-56

Query Match      100.0%; Score 370; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFSCCRDTSATPOSASIKALRNANLRDSSNHLTDLYRRDETIQVKG 60
DB      1 MHRLLFVYTLICANFSCCRDTSATPOSASIKALRNANLRDSSNHLTDLYRRDETIQVKG 60
QY      61 NGVOSPREPNSYPRLNLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEDIS 120
DB      61 NGVOSPREPNSYPRLNLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEDIS 120
QY      121 ESTTIIRGMCCKHEVPRIKSRTNQIKTFKSDDYFVAKPGFKIYYSLLDPQPAASE 180
DB      121 ESTTIIRGMCCKHEVPRIKSRTNQIKTFKSDDYFVAKPGFKIYYSLLDPQPAASE 180
QY      121 TWESVTSSISGVSYNSPSVTDPDLIADALDKKIAEFDVEDLLKYNFESWQEDLENNY 240
DB      121 TWESVTSSISGVSYNSPSVTDPDLIADALDKKIAEFDVEDLLKYNFESWQEDLENNY 240
QY      241 LPTPRYGRGSHYDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
DB      241 LPTPRYGRGSHYDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
QY      301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB      301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370

RESULT 4
US-09-876-813-2
; Sequence 2, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGPA
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-05-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-813-2

Query Match      100.0%; Score 370; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFSCCRDTSATPOSASIKALRNANLRDSSNHLTDLYRRDETIQVKG 60
DB      1 MHRLLFVYTLICANFSCCRDTSATPOSASIKALRNANLRDSSNHLTDLYRRDETIQVKG 60
QY      61 NGVOSPREPNSYPRLNLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEDIS 120
DB      61 NGVOSPREPNSYPRLNLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEDIS 120
QY      121 ESTTIIRGMCCKHEVPRIKSRTNQIKTFKSDDYFVAKPGFKIYYSLLDPQPAASE 180
DB      121 ESTTIIRGMCCKHEVPRIKSRTNQIKTFKSDDYFVAKPGFKIYYSLLDPQPAASE 180
QY      181 TWESVTSSISGVSYNSPSVTDPDLIADALDKKIAEFDVEDLLKYNFESWQEDLENNY 240
DB      181 TWESVTSSISGVSYNSPSVTDPDLIADALDKKIAEFDVEDLLKYNFESWQEDLENNY 240
QY      241 LPTPRYGRGSHYDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
DB      241 LPTPRYGRGSHYDRKSKVLDRLNDDAKRYSCTPRYSVNIREELKLANVFFPRCLLVQ 300
QY      301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB      301 RCGNCGCGTVMWRSCCTCNSGKTVMKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY      361 DCICSSRPPR 370
DB      361 DCICSSRPPR 370

RESULT 5
US-09-833-245-1482
; Sequence 1482, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1482
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1482

Query Match      100.0%; Score 370; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MHRLLFVYTLICANFSCCRDTSATPOSASIKALRNANLRDSSNHLTDLYRRDETIQVKG 60
DB      1 MHRLLFVYTLICANFSCCRDTSATPOSASIKALRNANLRDSSNHLTDLYRRDETIQVKG 60
QY      61 NGVOSPREPNSYPRLNLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEDIS 120
DB      61 NGVOSPREPNSYPRLNLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEDIS 120
```

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Db 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLDFQPAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLDFQPAASE 180
Qy 181 TNWESVTSISGVSYNPSVTDPTLLADALDKKIAEFTVEDLLKYNFNPESWOEDLENNY 240
Db 181 TNWESVTSISGVSYNPSVTDPTLLADALDKKIAEFTVEDLLKYNFNPESWOEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKYVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPPRCCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKYVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPPRCCLLVQ 300
Qy 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
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RESULT 6

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US-10-086-623-8
; Sequence 8, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: Li, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: TUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Ane
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/448332
; CURRENT APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-623-8
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Query Match 100.0%; Score 370; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MHRLIFFVTLICANFCSCRDTSATPQASISAKLRNANLRDSESHLTLVYRDDETIQVKG 60
Db 1 MHRLIFFVTLICANFCSCRDTSATPQASISAKLRNANLRDSESHLTLVYRDDETIQVKG 60
Qy 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
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Qy 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLDFQPAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLDFQPAASE 180
Qy 181 TNWESVTSISGVSYNPSVTDPTLLADALDKKIAEFTVEDLLKYNFNPESWOEDLENNY 240
Db 181 TNWESVTSISGVSYNPSVTDPTLLADALDKKIAEFTVEDLLKYNFNPESWOEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKYVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPPRCCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKYVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPPRCCLLVQ 300
Qy 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
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RESULT 7

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US-10-139-583-37
; Sequence 37, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-37
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Query Match 100.0%; Score 370; DB 13; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MHRLIFFVTLICANFCSCRDTSATPQASISAKLRNANLRDSESHLTLVYRDDETIQVKG 60
Db 1 MHRLIFFVTLICANFCSCRDTSATPQASISAKLRNANLRDSESHLTLVYRDDETIQVKG 60
Qy 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
Db 61 NGYVSPFPNSYPRLNLLTWRLHSQENTRIQLVFDNQGLEAEANDICRYDFVEVEDIS 120
Qy 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLDFQPAASE 180
Db 121 ETSIIIRGMCQKHEVPRIKSRITNOIKITFKSDDYFVAKGPFKLYSLLDFQPAASE 180
Qy 181 TNWESVTSISGVSYNPSVTDPTLLADALDKKIAEFTVEDLLKYNFNPESWOEDLENNY 240
Db 181 TNWESVTSISGVSYNPSVTDPTLLADALDKKIAEFTVEDLLKYNFNPESWOEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKYVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPPRCCLLVQ 300
Db 241 LDTPRYGRSYHDKRSKYVDLRLNDADAKRYSCTPRNYSVNIREELKLANVVFPPRCCLLVQ 300
Qy 301 RCGNCGCGTVMWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERC 360
```

```
Db      301 RCGGNGCGCTVWNRSTCNSGKTVKKYHEVLQEPHGIKRRGAKTMALVDIOLDHHERC 360
      361 DCICSSRPPR 370
      361 DCICSSRPPR 370

Query Match
Best Local Similarity 100.0%; Score 370; DB 13; Length 370;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Publication No. US20020183273A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2
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Query Match
Best Local Similarity 100.0%; Score 370; DB 13; Length 370;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-039-847A-2
; Sequence 2, Application US/10039847A
; Publication No. US20020183273A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039,847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-847A-2
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US-10-260-539-8
; Sequence 8, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
; APPLICANT: NASE, Karin
; APPLICANT: LI, Xu-Li
; APPLICANT: FONTEN, Annica
; APPLICANT: UTELA, Marko
```

```
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES T
; FILE REFERENCE: 1064/448302
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-539-8
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Query Match
Best Local Similarity 100.0%; Score 370; DB 14; Length 370;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-264-361-5
; Sequence 5, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
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US-10-264-361-5
; Sequence 5, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
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;; CURRENT FILING DATE: 2002-10-03
;; PRIOR APPLICATION NUMBER: US/09/695,121
;; PRIOR FILING DATE: 2000-10-23
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 5
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-264-361-5

Query Match 100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOVKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOVKG 60
QY 61 NGYVQSPFPNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVDIS 120
DB 61 NGYVQSPFPNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFQPAASE 180
QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESMOEDLENNY 240
DB 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESMOEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBELKANVVFPPRCLLVQ 300
DB 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBELKANVVFPPRCLLVQ 300
QY 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 11
US-10-258-557-2
;; Sequence 2, Application US/10258557
;; Publication No. US20030100502A1
;; GENERAL INFORMATION:
;; APPLICANT: Beale, John
;; APPLICANT: Gonzalez-Demhitt, Patricia
;; APPLICANT: Hammond, Lisa
;; APPLICANT: Lu, Jirong
;; APPLICANT: Na, Songqing
;; APPLICANT: Su, Eric
;; APPLICANT: Wlitcher, Derrick
;; TITLE OF INVENTION: TREATING MUSCULOSKELETAL DISORDERS USING LP85 AND ANALOGS THEREOF
;; FILE REFERENCE: X-14392M
;; CURRENT APPLICATION NUMBER: US/10/258,557
;; CURRENT FILING DATE: 2002-10-23
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-258-557-2

Query Match 100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOVKG 60

DB 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOVKG 60
QY 61 NGYVQSPFPNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVDIS 120
DB 61 NGYVQSPFPNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFQPAASE 180
QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESMOEDLENNY 240
DB 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESMOEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBELKANVVFPPRCLLVQ 300
DB 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBELKANVVFPPRCLLVQ 300
QY 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
DB 301 RCGNCGCGTNNWRSCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY 361 DCICSSRPPR 370
DB 361 DCICSSRPPR 370

RESULT 12
US-10-226-559-2
;; Sequence 2, Application US/10226559
;; Publication No. US20030105015A1
;; GENERAL INFORMATION:
;; APPLICANT: Gilbertson, Debra G.
;; APPLICANT: Hart, Charles E.
;; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
;; FILE REFERENCE: 00-28
;; CURRENT APPLICATION NUMBER: US/10/226,559
;; CURRENT FILING DATE: 2002-08-23
;; PRIOR APPLICATION NUMBER: US/09/540,224
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: US 60/180,169
;; PRIOR FILING DATE: 2000-02-04
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-226-559-2

Query Match 100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOVKG 60
DB 1 MHRLLFYVTLICANFCSCRDTSATPOSASIKALRNANLRDSENLTLDRDETIOVKG 60
QY 61 NGYVQSPFPNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVDIS 120
DB 61 NGYVQSPFPNSYPRNLLTWRLHSQENTRIQLVFDNQGLEAENDICRYDFVEVDIS 120
QY 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFQPAASE 180
DB 121 ETSITIRGRWCGHKEVPPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFQPAASE 180
QY 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESMOEDLENNY 240
DB 181 TNWESVTSISGVSYNSPSVTDPTLIADALDKKIAEFTVEDLKYFNPESMOEDLENNY 240
QY 241 LDTPRYRGRSYHDRKSKVDLRLNDADAKRYSCPTPNYSVNI REBELKANVVFPPRCLLVQ 300

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Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Qy      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Db      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Qy      361 DCTCSSRPPR 370
Db      361 DCTCSSRPPR 370

RESULT 13
US-10-274-638-2
; Sequence 2, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; FILE REFERENCE: 01-30
; CURRENT APPLICATION NUMBER: US/10/274,638
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/346,117
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-638-2

Query Match      100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
Db      1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
Qy      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Db      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Qy      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEDPAAASE 180
Db      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEDPAAASE 180
Qy      181 TWVESTSSISGVSYNSPSVTDPTLLADALDKIAEFDVVEDELLKTFNPESWQEDLENMY 240
Db      181 TWVESTSSISGVSYNSPSVTDPTLLADALDKIAEFDVVEDELLKTFNPESWQEDLENMY 240
Qy      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Qy      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Db      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Qy      361 DCTCSSRPPR 370
Db      361 DCTCSSRPPR 370

RESULT 14
US-10-011-364-4
; Sequence 4, Application US/10011364
; Publication No. US20030153495A1
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henry
```

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; APPLICANT: Jeffers, Michael
; APPLICANT: Shinkete, Richard
; APPLICANT: Prayaga, Sushirdas
; APPLICANT: Boldog, Ferenc
; APPLICANT: Yang, Weijia
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Rittman, B.
; APPLICANT: Shinkete, Juliette
; APPLICANT: Larocheille, William
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth
; FILE REFERENCE: Factors
; CURRENT APPLICATION NUMBER: US/10/011,364
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/246,206
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 09/992,840
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-364-4

Query Match      100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
Db      1 MHRLLFYVTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLVRRDETIQVKG 60
Qy      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Db      61 NGVQSPRPFPNSYPRLLLTWRLHSGQENTRIQLVFNQGLGEAENDICRYDVEVEDIS 120
Qy      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEDPAAASE 180
Db      121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYYSLLDEDPAAASE 180
Qy      181 TWVESTSSISGVSYNSPSVTDPTLLADALDKIAEFDVVEDELLKTFNPESWQEDLENMY 240
Db      181 TWVESTSSISGVSYNSPSVTDPTLLADALDKIAEFDVVEDELLKTFNPESWQEDLENMY 240
Qy      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVSVNIRELKLAVVFFPRCLVQ 300
Qy      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Db      301 RCGNCGCGTVMNRSTCNSGKTVKKYHEVLOEPGHIKRGAKTMAVLDIOLDHHERC 360
Qy      361 DCTCSSRPPR 370
Db      361 DCTCSSRPPR 370

RESULT 15
US-10-277-802-56
; Sequence 56, Application US/10277802
; Publication No. US20030190707A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/10/277,802
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/915,582
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
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/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 60/179,065
/ PRIOR FILING DATE: 2000-01-31
/ PRIOR APPLICATION NUMBER: 60/180,628
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: 60/231,968
/ PRIOR FILING DATE: 2000-09-12
/ NUMBER OF SEQ ID NOS: 97
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO: 56
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-277-802-56

Query Match      100.0%; Score 370; DB 14; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSGCRDTSATPOSASIKALRNANLRDSESNHLLTDLRYRDETIQYKG 60
Db 1 MHRLLFYVTLICANFCSGCRDTSATPOSASIKALRNANLRDSESNHLLTDLRYRDETIQYKG 60

Qy 61 NGYVQSPFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

Qy 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
Db 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180

Qy 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLAKYFNPESWQEDLENNY 240
Db 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLAKYFNPESWQEDLENNY 240

Qy 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNVSVNIREEKLNAVVFPPRCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNVSVNIREEKLNAVVFPPRCLLVQ 300

Qy 301 RCGGCGGCTVNMWRSCTCNSGKTVKHYEVLOFEFGHKKRGRATMALVDIQLDHHERC 360
Db 301 RCGGCGGCTVNMWRSCTCNSGKTVKHYEVLOFEFGHKKRGRATMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 16
US-10-246-091-8
/ Sequence 8, Application US/10246091
/ Publication No. US20030203844A1
/ GENERAL INFORMATION:
/ APPLICANT: Dellani, Klotumars
/ APPLICANT: Jamson, Ann Marie
/ APPLICANT: Kuhn, Georg
/ APPLICANT: Plate, Karlheinz
/ APPLICANT: Schnazzer, Anne
/ APPLICANT: Wachus, Frank-Peter
/ APPLICANT: Zhao, Ming
/ TITLE OF INVENTION: Treatment of Central Nervous System Disorders
/ FILE REFERENCE: 21882-504 (PDGF/VEGF)
/ CURRENT APPLICATION NUMBER: US/10/246,091
/ PRIOR FILING DATE: 2002-09-18
/ PRIOR APPLICATION NUMBER: 60/323,381
/ PRIOR FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/326,044
/ PRIOR FILING DATE: 2001-09-28
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO: 8
/ LENGTH: 370
/ TYPE: PRT
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/ ORGANISM: Homo sapiens
US-10-246-091-8

Query Match      100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSGCRDTSATPOSASIKALRNANLRDSESNHLLTDLRYRDETIQYKG 60
Db 1 MHRLLFYVTLICANFCSGCRDTSATPOSASIKALRNANLRDSESNHLLTDLRYRDETIQYKG 60

Qy 61 NGYVQSPFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

Qy 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
Db 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180

Qy 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLAKYFNPESWQEDLENNY 240
Db 181 TNMESVTSSISGVSNPSVTDPTLIADALDKIAEFTVBDLAKYFNPESWQEDLENNY 240

Qy 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNVSVNIREEKLNAVVFPPRCLLVQ 300
Db 241 LDTPRYRGRSYHDRKSKYVDLRLNDADAKRYSCTPRNVSVNIREEKLNAVVFPPRCLLVQ 300

Qy 301 RCGGCGGCTVNMWRSCTCNSGKTVKHYEVLOFEFGHKKRGRATMALVDIQLDHHERC 360
Db 301 RCGGCGGCTVNMWRSCTCNSGKTVKHYEVLOFEFGHKKRGRATMALVDIQLDHHERC 360

Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 17
US-10-365-095-2
/ Sequence 2, Application US/10365095
/ Publication No. US20030224488A1
/ GENERAL INFORMATION:
/ APPLICANT: Fox, Brian A.
/ APPLICANT: Moore, Margaret D.
/ APPLICANT: Swiderek, Kristine M.
/ APPLICANT: Birks, Carl W.
/ TITLE OF INVENTION: MATERIALS AND METHODS FOR PREPARING DIMERIC GROWTH FACTORS
/ FILE REFERENCE: 01-33
/ CURRENT APPLICATION NUMBER: US/10/365,095
/ CURRENT FILING DATE: 2003-02-11
/ PRIOR APPLICATION NUMBER: 60/355,882
/ PRIOR FILING DATE: 2002-02-11
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-365-095-2

Query Match      100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRLLFYVTLICANFCSGCRDTSATPOSASIKALRNANLRDSESNHLLTDLRYRDETIQYKG 60
Db 1 MHRLLFYVTLICANFCSGCRDTSATPOSASIKALRNANLRDSESNHLLTDLRYRDETIQYKG 60

Qy 61 NGYVQSPFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPFPNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLBEAENDICRYDFVEVEDIS 120

Qy 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
Db 121 ETSITIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFPAKPGFKIYSLLEDFOPAAASE 180
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Db 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
Qy 181 TMEESVTSISISGVSYNSPVTDPPTLADALDKKIAEDTVEEDLLKYNPESMOEDLENNY 240
Db 181 TMEESVTSISISGVSYNSPVTDPPTLADALDKKIAEDTVEEDLLKYNPESMOEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYG 300
Db 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYG 300
Qy 301 RCGGNGCGGTVMNRSCCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVLDIOLDHHERC 360
Db 301 RCGGNGCGGTVMNRSCCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVLDIOLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 18
US-10-321-962-4
; Sequence 4, Application US/10321962
; Publication No. US2004006015A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Fernandes, Elma
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Larochele, William J.
; APPLICANT: Lichenstein, Henry S.
; APPLICANT: Peterson, Jeffrey
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Rittman, Bech
; APPLICANT: Shimkets, Uliette
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Yang, MeiJia
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
; TITLE OF INVENTION: Using Growth Factors
; FILE REFERENCE: 15966-557A 1BD CIP2
; CURRENT APPLICATION NUMBER: US/10/321,962
; CURRENT FILING DATE: 2002-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: CureSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-962-4

Query Match 100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRILFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
Db 1 MHRILFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
Qy 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Qy 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
Db 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
Qy 181 TMEESVTSISISGVSYNSPVTDPPTLADALDKKIAEDTVEEDLLKYNPESMOEDLENNY 240
Db 181 TMEESVTSISISGVSYNSPVTDPPTLADALDKKIAEDTVEEDLLKYNPESMOEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYG 300
Db 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYG 300

Qy 301 RCGGNGCGGTVMNRSCCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVLDIOLDHHERC 360
Db 301 RCGGNGCGGTVMNRSCCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVLDIOLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 19
US-10-606-055-2
; Sequence 2, Application US/10606055
; Publication No. US20040043027A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/10/606,055
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US/09/808,972
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-606-055-2

Query Match 100.0%; Score 370; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHRILFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
Db 1 MHRILFVYTLICANFSCSDTSATPOSASIKALRNANLRDESNHLLTDLYRDETIQVKG 60
Qy 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Db 61 NGVQSPRPENSYPRNLLTWRLHSEENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Qy 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
Db 121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDDYFVAKPGFKIYSLLEDFQPAASE 180
Qy 181 TMEESVTSISISGVSYNSPVTDPPTLADALDKKIAEDTVEEDLLKYNPESMOEDLENNY 240
Db 181 TMEESVTSISISGVSYNSPVTDPPTLADALDKKIAEDTVEEDLLKYNPESMOEDLENNY 240
Qy 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYG 300
Db 241 LDTPRYGRSYHDKRSKVDLDRINDAKRYSCTPRNYSVNIIRBELKLANVFFPRCLLYG 300
Qy 301 RCGGNGCGGTVMNRSCCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVLDIOLDHHERC 360
Db 301 RCGGNGCGGTVMNRSCCTCNSGKTVKKYHEVLOFEPGHIKRGRAKTMALVLDIOLDHHERC 360
Qy 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

Db 361 DCICSSRPR 370

RESULT 20

US-10-664-432-5

Sequence 5, Application US/10664432

Publication No. US20040043031A1

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE.

FILE REFERENCE: 00-12

CURRENT APPLICATION NUMBER: US/10/664,432

CURRENT FILING DATE: 2003-09-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 370

TYPE: PR

ORGANISM: Homo sapiens

US-10-664-432-5

Query Match 100.0%; Score 370; DB 15; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLFFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLRRDETIOYKG 60

Db 1 MHRLFFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLRRDETIOYKG 60

QY 61 NGVOSPRFPNSYPRLNLLTWRLHSEENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

Db 61 NGVOSPRFPNSYPRLNLLTWRLHSEENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

QY 121 ESTTIRRCWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

Db 121 ESTTIRRCWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

QY 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNESQOEDLENNY 240

Db 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNESQOEDLENNY 240

QY 241 IDTPRYGRSYHDRSKYVDLRLNDAKRYSCTPRANYSVINREBLKANVVEFPCLVQ 300

Db 241 IDTPRYGRSYHDRSKYVDLRLNDAKRYSCTPRANYSVINREBLKANVVEFPCLVQ 300

QY 301 RCGNCGCGCTVNMRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERC 360

Db 301 RCGNCGCGCTVNMRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERC 360

QY 361 DCICSSRPR 370

Db 361 DCICSSRPR 370

RESULT 21

US-10-650-284-2

Sequence 2, Application US/10650284

Publication No. US20040110683A1

GENERAL INFORMATION:

APPLICANT: Hui, Rutai

APPLICANT: Chen, Jingzhou

APPLICANT: Liu, Baohua

APPLICANT: Liu, Yuchang

TITLE OF INVENTION: Cell Proliferation Factor Fwa267

FILE REFERENCE: 043774/268252

CURRENT APPLICATION NUMBER: US/10/650,284

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: CN01109260.2

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 370

TYPE: PR

ORGANISM: Homo sapiens

US-10-650-284-2

Query Match 100.0%; Score 370; DB 16; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLFFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLRRDETIOYKG 60

Db 1 MHRLFFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLRRDETIOYKG 60

QY 61 NGVOSPRFPNSYPRLNLLTWRLHSEENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

Db 61 NGVOSPRFPNSYPRLNLLTWRLHSEENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

QY 121 ESTTIRRCWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

Db 121 ESTTIRRCWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

QY 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNESQOEDLENNY 240

Db 181 TMESVTSISGVSNSPSVTDPTLIADALDKKIAEFTVEDLKYFNESQOEDLENNY 240

QY 241 IDTPRYGRSYHDRSKYVDLRLNDAKRYSCTPRANYSVINREBLKANVVEFPCLVQ 300

Db 241 IDTPRYGRSYHDRSKYVDLRLNDAKRYSCTPRANYSVINREBLKANVVEFPCLVQ 300

QY 301 RCGNCGCGCTVNMRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERC 360

Db 301 RCGNCGCGCTVNMRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERC 360

QY 361 DCICSSRPR 370

Db 361 DCICSSRPR 370

RESULT 22

US-10-664-432-5

Sequence 5, Application US/10664432

Publication No. US20040228870A9

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE.

FILE REFERENCE: 00-12

CURRENT APPLICATION NUMBER: US/10/664,432

CURRENT FILING DATE: 2003-09-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 370

TYPE: PR

ORGANISM: Homo sapiens

US-10-664-432-5

Query Match 100.0%; Score 370; DB 16; Length 370;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHRLFFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLRRDETIOYKG 60

Db 1 MHRLFFVYTLICANFCSCRDTSATPQASIKALRNANLRDPSNHLTDLRRDETIOYKG 60

QY 61 NGVOSPRFPNSYPRLNLLTWRLHSEENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

Db 61 NGVOSPRFPNSYPRLNLLTWRLHSEENTRIQLVFDNQGLEAENDICRYDFVEVEDIS 120

QY 121 ESTTIRRCWCGHKEVPRIKSRITNOIKITFKSDDYFVAKGFKIYSLLEDFOPAASE 180

```

Db      121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
QY      181 TWMEVTSISGVSNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESQEDLENNY 240
Db      181 TWMEVTSISGVSNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESQEDLENNY 240
QY      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVNIREELKLANVFFPRCLLVQ 300
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVNIREELKLANVFFPRCLLVQ 300
QY      301 RCGGNCGGCTVWNRSCCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db      301 RCGGNCGGCTVWNRSCCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY      361 DCICSSRPPR 370
Db      361 DCICSSRPPR 370

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RESULT 23 US-10-877-623-2

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; Sequence 2, Application US/10877623
; Publication No. US20040242850A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZWGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/10/877,623
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-877-623-2

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Query Match 100.0%; Score 370; DB 16; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MHRLLFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVG 60
Db      1 MHRLLFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVG 60
QY      61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Db      61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
QY      121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
Db      121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
QY      181 TWMEVTSISGVSNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESQEDLENNY 240
Db      181 TWMEVTSISGVSNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESQEDLENNY 240
QY      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVNIREELKLANVFFPRCLLVQ 300
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVNIREELKLANVFFPRCLLVQ 300

```

```

QY      301 RCGGNCGGCTVWNRSCCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db      301 RCGGNCGGCTVWNRSCCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY      361 DCICSSRPPR 370
Db      361 DCICSSRPPR 370

```

RESULT 24 US-10-772-927A-9

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; Sequence 9, Application US/10772927A
; Publication No. US20040248796A1
; GENERAL INFORMATION:
; APPLICANT: Aitalo, et al.
; TITLE OF INVENTION: VEGF-B AND PDGF MODULATION OF STEM CELLS
; FILE REFERENCE: 28967/39140B
; CURRENT APPLICATION NUMBER: US/10/772,927A
; PRIOR FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US 60/445,021
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/471,412
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-772-927A-9

```

Query Match 100.0%; Score 370; DB 16; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MHRLLFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVG 60
Db      1 MHRLLFVYLLICANFCSCRDTSATPOSASIKALRNANLRDSENNHLDLYRRDETIOVG 60
QY      61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
Db      61 NGVOSPRFPNSYPNNLLTWRLHSQENTRIQLVFNQGLBEAENDICRYDFVEVEDIS 120
QY      121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
Db      121 ESTTIRGRWCGHKEVPRIKSRITNOIKITFKSDYFVAKPGFKIYSLLEDFOPAAASE 180
QY      181 TWMEVTSISGVSNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESQEDLENNY 240
Db      181 TWMEVTSISGVSNSPSVTDPTLIADALDKKIAEFDTVEDLLKYNFESQEDLENNY 240
QY      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVNIREELKLANVFFPRCLLVQ 300
Db      241 LDTPRYGRSYPHDKSKVDLDRNDADAKRYSCTPRNVNIREELKLANVFFPRCLLVQ 300
QY      301 RCGGNCGGCTVWNRSCCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db      301 RCGGNCGGCTVWNRSCCTNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
QY      361 DCICSSRPPR 370
Db      361 DCICSSRPPR 370

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RESULT 25 US-10-910-938-2

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; Sequence 2, Application US/10910938
; Publication No. US20050031694A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; LIGAMENT AND CARTILAGE USING ZWGF4

```

```
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/10/910,938
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US/10/226,559
; PRIOR FILING DATE: 2003-08-23
; PRIOR APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-938-2
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Query Match 100.0%; Score 370; DB 17; Length 370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 MHRLEFVYTLICANFCSCDTSATPOSASIKALRNANLRDESNHITDLYRDETIQYKG 60
Db 1 MHRLEFVYTLICANFCSCDTSATPOSASIKALRNANLRDESNHITDLYRDETIQYKG 60
OY 61 NGYVQSPRFPNSYPNNLLLTWRHLSQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
Db 61 NGYVQSPRFPNSYPNNLLLTWRHLSQENTRIQLVFNQFGLBEAENDICRYDFVEVEDIS 120
OY 121 ETSITIRGRWCGHKEVPRIKRTNQIKITFKSDIYFVAKPGFKIYYSLEDFOPAAASE 180
Db 121 ETSITIRGRWCGHKEVPRIKRTNQIKITFKSDIYFVAKPGFKIYYSLEDFOPAAASE 180
OY 181 TNMESVTSISGVSYNSPSVTPTLIADALDKKIAEFTVEDLTKYFNPESWQEDLENNY 240
Db 181 TNMESVTSISGVSYNSPSVTPTLIADALDKKIAEFTVEDLTKYFNPESWQEDLENNY 240
OY 241 LDTPRYRGRSYHDKRSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPRCLLVQ 300
Db 241 LDTPRYRGRSYHDKRSKYDLDRINDAKRYSCTPRNYSVINIREELKLANVVFPRCLLVQ 300
OY 301 RCGGNCGGCTVWMBCTCNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
Db 301 RCGGNCGGCTVWMBCTCNSGKTVKKYHEVLOFEPGHIKRRGRAKTMALVDIQLDHHERC 360
OY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370
```

Search completed: November 10, 2005, 09:51:13
Job time : 167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2005, 09:36:17 ; Search time 40 seconds

(without alignments)
890.005 Million cell updates/sec

Title: US-10-606-055-2

Perfect score: 370

Sequence: 1 MHRLLFVYLLICANFCSCRD.....DIQLDHERRCDCICSRPPR 370

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 5

Total number of hits satisfying chosen parameters: 19093

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 100 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	269	72.7	370	2	JC7591	spinal cord-deri
2	32	8.6	370	2	JC7592	spinal cord-deri
3	27	7.3	370	2	JC7998	platelet-derived g
4	8	2.2	77	2	S37239	metallochionein-11
5	8	2.2	77	2	S52636	metallochionein -
6	8	2.2	79	2	TQ2128	metallochionein -
7	8	2.2	80	2	TQ2063	metallochionein-11
8	8	2.2	80	2	TQ3404	metallochionein-11
9	8	2.2	80	2	T12326	metallochionein
10	8	2.2	80	2	T14387	metallochionein-11
11	8	2.2	80	2	T10087	metallochionein -
12	8	2.2	81	1	SMUTL	metallochionein-11
13	8	2.2	81	2	S57861	metallochionein 2a
14	8	2.2	82	2	TQ7114	metallochionein-11
15	8	2.2	82	2	TQ7076	metallochionein ty
16	8	2.2	82	2	TQ3727	metallochionein-11
17	8	2.2	84	2	TQ3787	metallochionein-11
18	8	2.2	353	2	AB1284	aminopeptidase P h
19	8	2.2	353	2	AF1606	aminopeptidase P h
20	8	2.2	485	1	B37855	glucose-6-phosphat
21	8	2.2	531	2	TQ1415	basic leucine zipp
22	8	2.2	995	2	AB1398	formate dehydrogen
23	8	2.2	995	2	AE1773	formate dehydrogen
24	8	2.2	1138	1	S24066	protein-tyrosine k
25	7	1.9	153	2	G90831	probable endopepti
26	7	1.9	155	2	B90571	probable endopepti
27	7	1.9	155	2	C85744	probable endopepti
28	7	1.9	171	2	T10904	sporamin - sweet p
29	7	1.9	172	1	RKR25	ribosamin-bisphosp

30	7	1.9	174	2	H96688	hypothetical prote
31	7	1.9	175	1	RKR256	ribose-bisphosph
32	7	1.9	175	1	RKR259	ribose-bisphosph
33	7	1.9	175	2	TQ2060	hypothetical prote
34	7	1.9	181	2	A71145	hypothetical prote
35	7	1.9	238	2	T48888	probable phosphor
36	7	1.9	245	2	A99163	dipeptide transpor
37	7	1.9	245	2	AH3124	hypothetical prote
38	7	1.9	274	2	A71140	hypothetical prote
39	7	1.9	280	2	H72504	hypothetical prote
40	7	1.9	291	2	T34043	hypothetical prote
41	7	1.9	326	2	A70368	conserved hypothet
42	7	1.9	329	2	B84199	hypothetical prote
43	7	1.9	384	2	S38232	glucose kinase glk
44	7	1.9	335	2	A10878	conserved hypothet
45	7	1.9	346	2	A34365	holocytochrome-c s
46	7	1.9	361	2	T39723	Grpase activating
47	7	1.9	363	2	C75387	ketol-acid reducto
48	7	1.9	384	2	S38232	hypothetical prote
49	7	1.9	405	2	AE0990	probable membrane
50	7	1.9	410	2	AE2621	conserved hypothet
51	7	1.9	410	2	E97403	hypothetical prote
52	7	1.9	419	1	S47692	hypothetical 43.8k
53	7	1.9	419	2	B91169	probable transport
54	7	1.9	419	2	B86015	probable transport
55	7	1.9	497	2	B97729	heat shock protein
56	7	1.9	500	2	B86306	F20D23.26 protein
57	7	1.9	506	1	W2W47	E2 protein - human
58	7	1.9	510	2	B60280	bacillolysin-like
59	7	1.9	510	2	A60280	zinc metalloprotei
60	7	1.9	510	2	AD1100	phycoene dehydroge
61	7	1.9	524	2	A32617	hypothetical prote
62	7	1.9	565	2	TQ2899	hypothetical prote
63	7	1.9	580	2	S56645	chaperonin 60. alpi
64	7	1.9	588	2	I40725	2-isopropylmalate
65	7	1.9	644	2	S63056	probable membrane
66	7	1.9	647	1	S42939	malate dehydrogena
67	7	1.9	679	2	H96813	hypothetical prote
68	7	1.9	749	2	E71275	hypothetical integ
69	7	1.9	772	2	S32859	integrin beta 2 ch
70	7	1.9	931	2	E70140	hypothetical prote
71	7	1.9	1010	2	AH2553	hypothetical prote
72	7	1.9	1086	2	S74251	phosphorylase kin
73	7	1.9	1093	2	S74250	phosphorylase kin
74	7	1.9	1134	2	TQ4587	hypothetical prote
75	7	1.9	1192	2	G70513	5-methyltetrahydro
76	7	1.9	1276	2	F83086	hypothetical prote
77	7	1.9	1359	2	S49883	nuclear protein ST
78	7	1.9	1792	2	T13939	myosin V - fruit f
79	7	1.9	1971	2	S27938	hypothetical prote
80	7	1.9	1957	2	S68453	sodium channel pro
81	7	1.9	3712	2	S18253	lamtin alpha-1 ch
82	7	1.9	34	2	H53480	melanoma antigen-s
83	6	1.6	53	2	S77865	ribosomal protein
84	6	1.6	59	2	H69463	hypothetical prote
85	6	1.6	61	2	D90879	hypothetical prote
86	6	1.6	61	2	F85739	hypothetical prote
87	6	1.6	64	2	A106P2	phage shock protei
88	6	1.6	72	1	A106P2	phage shock protei
89	6	1.6	74	2	T17834	hypothetical prote
90	6	1.6	75	2	E72681	hypothetical prote
91	6	1.6	78	2	T28903	hypothetical prote
92	6	1.6	82	2	C48349	ul28 protein - gsa
93	6	1.6	83	2	S17145	6-phosphofructo-2-
94	6	1.6	83	2	E81896	hypothetical prote
95	6	1.6	87	2	E83296	hypothetical prote
96	6	1.6	93	2	D69262	hypothetical prote
97	6	1.6	93	2	AF1331	hypothetical prote
98	6	1.6	93	2	AF1702	hypothetical prote
99	6	1.6	96	2	UQ2011	hypothetical 11k p
100	6	1.6	98	2	T42307	hypothetical prote

ALIGNMENTS

RESULT 1

spinal cord-derived growth factor-B precursor - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07591
R/Hamada, T.; Uti-Rei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A/Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDFG/PDGF-C/
A/Reference number: J07591; MUID:21092670; PMID:11162582
A/Accession: J07591
A/Molecule type: DNA
A/Residues: 1-370 <HAM>
A/Cross-references: UNIPROT:Q9BWV5; UNIPROT:Q9GZP0; DDBJ:AB033832
C/Genetics:
A/Gene: scdGF-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F:294-308/Region: conserved motif #status predicted

Query Match 72.7%: Score 269; DB 2; Length 370;

Best Local Similarity 99.7%: Pred. No. 1.6e-275; Matches 369; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLVREDETIOYKG	60
Db	1	MRLIFVYTLICANFCSCRDTSATPQASIKALRNANLRDESNHLLTDLVREDETIOYKG	60
Qy	61	NGYVSPFPFNYPNNLLTWLHSEENTRIQLVNDNQGLEAENDICRYFVEVDIS	120
Db	61	NGYVSPFPFNYPNNLLTWLHSEENTRIQLVNDNQGLEAENDICRYFVEVDIS	120
Qy	121	ESTTIIRGMCCHKVPPRIKSRITNOIKITFKSDYFVAKPGFKIYSLIEDFOFAASE	180
Db	121	ESTTIIRGMCCHKVPPRIKSRITNOIKITFKSDYFVAKPGFKIYSLIEDFOFAASE	180
Qy	161	TNWSVTSSISGVSYNSPSVTDPTLIADLADKIAEPDVEDLLKYFNPESWQEDLENNY	240
Db	161	TNWSVTSSISGVSYNSPSVTDPTLIADLADKIAEPDVEDLLKYFNPESWQEDLENNY	240
Qy	241	LDPTRYRGRSYDRSKYDLDRLNDAKRYSCTPPNYSNIRBEIKLANVFPFRCCLVQ	300
Db	241	LDPTRYRGRSYDRSKYDLDRLNDAKRYSCTPPNYSNIRBEIKLANVFPFRCCLVQ	300
Qy	301	RCGGNCGCGTWNRSCTCNSGKTVKRYHEVLQFEFGHTRGRGAKTMALVDIQLDHHERC	360
Db	301	RCGGNCGCGTWNRSCTCNSGKTVKRYHEVLQFEFGHTRGRGAKTMALVDIQLDHHERC	360
Qy	361	DCICSSRPPR 370	
Db	361	DCICSSRPPR 370	

RESULT 2

spinal cord-derived growth factor-B precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07592
R/Hamada, T.; Uti-Rei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A/Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDFG/PDGF-C/
A/Reference number: J07591; MUID:21092670; PMID:11162582
A/Contents: Fetal brain
A/Accession: J07592
A/Molecule type: mRNA
A/Residues: 1-370 <HAM>
A/Cross-references: UNIPROT:Q9EQT1; DDBJ:AB052170

C/Genetics:
A/Gene: scdGF-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F:294-308/Region: conserved motif #status predicted

Query Match 8.6%: Score 32; DB 2; Length 370;

Best Local Similarity 100.0%: Pred. No. 2.6e-25; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	23	ATPQASIKALRNANLRDESNHLLTDLVRRDE	54
Db	23	ATPQASIKALRNANLRDESNHLLTDLVRRDE	54

RESULT 3

platelet-derived growth factor-D - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C/Accession: J07998
R/Zhuo, Y.; Hoyle, G.W.; Zhang, J.; Morris, G.; Laaky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A/Title: A novel murine PDGF-D splicing variant results in significant differences in pe
A/Reference number: J07998; PMID:12890490
A/Accession: J07998
A/Genetics:
A/Molecule type: mRNA
A/Residues: 1-370 <ZHU>
C/Comment: This protein is a potent mesenchymal cell mitogen and chemotactant involve
A/Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C/Keywords: Fibrinosis; PDGF-D

Query Match 7.3%: Score 27; DB 2; Length 370;

Best Local Similarity 100.0%: Pred. No. 5e-20; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	142	SRTNQIKITFKSDDYFVAKPGFKIYYS	168
Db	142	SRTNQIKITFKSDDYFVAKPGFKIYYS	168

RESULT 4

metallothionein-like protein - white clover
C/Species: Trifolium repens (white clover)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S37239
R/Ellison, N.W.
Submitted to the EMBL Data Library, September 1993
A/Description: Sequence analysis of two cDNA clones for metallothionein-like proteins fr
A/Reference number: S37239
A/Accession: S37239
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-77 <ELL>
A/Cross-references: UNIPROT:P43398; EMBL:Z26492; NID:g403326; PIDN:CAA81264.1; PID:g4033
C/Superfamily: metallothionein

Query Match 2.2%: Score 8; DB 2; Length 77;

Best Local Similarity 100.0%: Pred. No. 1.5; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	302	CGGNCGCG 309	
Db	4	CGGNCGCG 11	

RESULT 5

S52636

metallothionein - fava bean
C/Species: Vicia faba (fava bean)
C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S52636
R/Polley, R.C.; Singh, K.B.
Plant Mol. Biol. 26, 435-444, 1994
A/Title: Isolation of a Vicia faba metallothionein-like gene: expression in foliar trieh
A/Reference number: S52636; MID:95036014; PMID:7948889
A/Accession: S52636
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-77 <POL>
A/Cross-references: UNIPROT:Q41657; EMBL:X77254; NID:G747905; PIDN:CA54471.1; PID:G7479
C/Superfamily: metallothionein

Query Match 2.2%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGG 309
DB 4 CGGNCGG 11

RESULT 6
JQ2128
metallothionein - soybean
C/Species: Glycine max (soybean)
C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: JQ2128
R/Kawashima, I.; Inokuchi, Y.; Chino, M.; Kimura, M.; Shimizu, N.
Plant Cell Physiol. 32, 913-916, 1991
A/Title: Isolation of a gene for a metallothionein-like protein from soybean.
A/Reference number: JQ2128
A/Accession: JQ2128
A/Molecule type: mRNA
A/Residues: 1-79 <KAW>
A/Cross-references: UNIPROT:Q7M213
A/Experimental source: seedling, cv. Saxa
C/Comment: This protein participates in detoxification and metabolism of heavy metals ch
C/Superfamily: metallothionein
C/Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGG 309
DB 4 CGGNCGG 11

RESULT 7
T02063
metallothionein-like protein - rice
C/Species: Oryza sativa (rice)
C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C/Accession: T02063
R/lee, M.C.; Kim, C.S.; Eun, M.Y.
submitted to the EMBL Data Library, August 1997
A/Description: Characterization of metallothionein-like protein from rice.
A/Reference number: Z14532
A/Accession: T02063
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <LEE>
A/Cross-references: UNIPROT:Q22488; EMBL:AF017365; NID:G2407284; PIDN:AAB70545.1; PID:G2
C/Superfamily: metallothionein

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGG 309
DB 4 CGGNCGG 11

RESULT 8
T03404
metallothionein-like protein - rice
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03404
R/Yu, L.H.; Umeda, M.; Liu, J.Y.; Zhao, N.M.; Uchimiyu, H.
Gene 206, 29-35, 1998
A/Title: A novel MT gene of rice plants is strongly expressed in the node portion of th
A/Reference number: Z14935; MID:98121509; PMID:9461411
A/Accession: T03404
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <YUL>
A/Cross-references: UNIPROT:Q04107; EMBL:AB002820; NID:G1944204; PIDN:BA19661.1; PID:G1
C/Superfamily: metallothionein

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGG 309
DB 4 CGGNCGG 11

RESULT 9
T12326
metallothionein - common ice plant
C/Species: Mesembryanthemum crystallinum (common ice plant)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C/Accession: T12326
R/Michalowski, C.B.; Bohner, H.J.
submitted to the EMBL Data Library, July 1998
A/Description: A metallothionein homolog from the ice plant Mesembryanthemum crystallinu
A/Reference number: Z17493
A/Accession: T12326
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <MIC>
A/Cross-references: UNIPROT:Q04688; EMBL:AF076912; NID:G3342197; PID:G3342198
C/Superfamily: metallothionein
C/Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGG 309
DB 4 CGGNCGG 11

RESULT 10
T14387
metallothionein-like protein - turnip
C/Species: Brassica rapa (turnip)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14387
R/Kim, H.U.; Kim, J.B.; Yun, C.H.; Kang, S.K.; Chung, T.Y.
Plant Physiol. 108, 863, 1995
A/Title: Nucleotide sequence of cDNA clone encoding a metallothionein-like protein from
A/Reference number: Z18022; MID:95534519; PMID:7610190
A/Accession: T14387
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <KIM>

A:Cross-references: UNIPROT:Q9269, EMBL:IJ1940, NID:g967969, PIDN:AAA74958.1, PID:g9679
A:Experimental source: subspecies pekinesis; flower
C:Function:
A:Description: participates in detoxification of heavy metals through metal-thiol binding
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGNCGCG 309
Db 4 CGNCGCG 11

RESULT 11

metallothionein - castor bean
C:Species: Ricinus communis (castor bean)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10087
R:Vangala, S.; Bailey-Serres, J.
Plant Physiol. 109, 721, 1995
A>Title: Nucleotide sequence of a maize (Zea mays L.) cDNA (Accession No. U29383) coding
A:Reference number: Z16941; MUID:96030260; PMID:7480354
A:Accession: T10087
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-80 <VAN>
A:Cross-references: UNIPROT:P30564, EMBL:I02306, NID:g169712, PID:g169713
A:Experimental source: strain Carmencita; tissue-type cotyledon
C:Genetics:
A:Gene: MTI
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGNCGCG 309
Db 4 CGNCGCG 11

RESULT 12

metallothionein-like protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: S18069, S57897
R:Takahashi, K.
submitted to the EMBL Data Library, October 1991
A:Reference number: S18069
A:Accession: S18069
A:Molecule type: mRNA
A:Residues: 1-81 <TAA>
A:Cross-references: UNIPROT:P25860, EMBL:X62818, NID:g16183, PIDN:CAA44630.1, PID:g16184
A:Experimental source: strain Columbia
R:Takahashi, K.
submitted to the EMBL Data Library, July 1992
A:Reference number: S57897
A:Accession: S57897
A:Molecule type: DNA
A:Residues: 1-81 <TAA>
A:Cross-references: EMBL:DJ1394, NID:g217856, PIDN:BA01990.1, PID:g217857
C:Genetics:
A:Introns: 22/2
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 1; Length 81;

Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGNCGCG 309
Db 4 CGNCGCG 11

RESULT 13

metallothionein 2a - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57861
R:Zhou, J.; Goldsborough, P.B.
Mol. Gen. Genet. 248, 318-328, 1995
A>Title: Structure, organization and expression of the metallothionein gene family in Ar
A:Reference number: S57858; MUID:9604699; PMID:7565594
A:Accession: S57861
A:Molecule type: DNA
A:Residues: 1-81 <ZHO>
A:Cross-references: UNIPROT:P25860
C:Genetics:
A:Gene: MT2a
A:Map position: III
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGNCGCG 309
Db 4 CGNCGCG 11

RESULT 14

metallothionein-like protein - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07114
R:Gitlich, A.; Ganai, M.; Stephan, U.W.; Baumelein, H.
Plant Mol. Biol. 37, 701-714, 1998
A>Title: Structure, expression and chromosomal localization of the metallothionein-like
A:Reference number: Z15923; MUID:96349862; PMID:9687073
A:Accession: T07114
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-82 <GIR>
A:Cross-references: UNIPROT:Q40158, EMBL:Z68138, NID:g1103688, PIDN:CAA92243.1, PID:g110
A:Experimental source: cultivar Bonner Best; root
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGNCGCG 309
Db 4 CGNCGCG 11

RESULT 15

metallothionein type II B - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07076
R:Whitelaw, C.A.; LeHuquet, J.A.; Thurman, D.A.; Tomsett, A.B.
submitted to the EMBL Data Library, July 1996

A:Description: The isolation and characterization of type II metallochionein-like genes
A:Reference number: Z15900
A:Accession: T03727
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-82 <WHI>
A:Cross-references: UNIPROT:Q40158; EMBL:L77966; NID:g1449137; PIDN:AA04675.1; PID:g144
A:Experimental source: strain A11a cralg
C:Genetics:
A:Gene: MTB
A:Introns: 22/2
C:Superfamily: metallochionein
C:Keywords: metal binding

Query Match 2.2%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
DB 4 CGGNCGGC 11

RESULT 16
T03727
metallochionein-like protein - rice
C:Species: Oryza sativa (rice)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03727
R:Chen, W.M.; Hsieh, H.M.; Huang, P.C.
A:Description: Signification of two introns in type 2 rice metallochionein-like gene.
A:Reference number: Z15032
A:Accession: T03727
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <CHE>
A:Cross-references: UNIPROT:P94029; EMBL:D89931; PIDN:BA014038.1
A:Experimental source: cv. Tainung 67, root
C:Genetics:
A:Gene: rGMT-2
A:Introns: 22/2; 48/2
C:Superfamily: metallochionein

Query Match 2.2%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
DB 4 CGGNCGGC 11

RESULT 17
T03787
metallochionein-like protein - rice
C:Species: Oryza sativa (rice)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03787
R:Lee, M.C.; Park, J.Y.; Kim, Y.H.; Sun, M.Y.
A:Description: Molecular cloning and characterization of metallochionein-like protein in
A:Reference number: Z15085
A:Accession: T03787
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-84 <LEB>
A:Cross-references: UNIPROT:P93433; EMBL:Y08529; PIDN:CA069845.1
C:Superfamily: metallochionein

Query Match 2.2%; Score 8; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 CGGNCGGC 309
DB 4 CGGNCGGC 11

RESULT 18
AB1244
aminopeptidase P homolog lmo1354 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB1244
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Jones, L.M.; Karsch, U.
Science 294, 849-852, 2001
A:Authors: Kreft, U.; Kuhn, M.; Kunet, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1244
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <GLA>
A:Cross-references: UNIPROT:Q8Y7C9; GB:NC_003210; PIDN:CAC99432.1; PID:g16410770; GSPDB
C:Experimental source: strain EGD-e
A:Gene: lmo1354
C:Superfamily: X-Pro aminopeptidase

Query Match 2.2%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 FDTVEDLL 224
DB 76 FDTVEDLL 83

RESULT 19
AF1606
aminopeptidase P homolog lmi1391 [imported] - Listeria innocua (strain C11p11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1606
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Jones, L.M.; Karsch, U.
Science 294, 849-852, 2001
A:Authors: Kreft, U.; Kuhn, M.; Kunet, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1606
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <GLA>
A:Cross-references: UNIPROT:Q92C00; GB:AL592022; PIDN:CAC96622.1; PID:g16413864; GSPDB:
A:Experimental source: strain C11p11262
C:Genetics:
A:Gene: lmi1391
C:Superfamily: X-Pro aminopeptidase

Query Match 2.2%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 FDTVEDLL 224
DB 76 FDTVEDLL 83

RESULT 20

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B37855
glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Zymomonas mobilis
C:Species: Zymomonas mobilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B37855
R:Barnell, W.O.; Yi, K.C.; Conway, T.
J. Bacteriol. 172, 7227-7240, 1990
A:Title: Sequence and genetic organization of a Zymomonas mobilis gene cluster that enc
A:Reference number: A37855; MUID:91072278; PMID:2254282
A:Accession: B37855
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485 <BAR>
A:Cross-references: UNIPROT:P21907; GB:M60615; GB:M37982; NID:g155589; PIDN:AAA27692.1;
C:Superfamily: glucose-6-phosphate dehydrogenase
C:Keywords: oxidoreductase

Query Match      2.2%; Score 8; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 DRLNDADK 268
DB      69 DRLNDADK 76

RESULT 21
T01415
basic leucine zipper protein - maize
C:Species: Zea mays (maize)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01415
R:Malsh, J.; Waters, C.A.; Freeling, M.
Genes Dev. 12, 208-218, 1998
A:Title: The maize gene l1guleless2 encodes a basic leucine zipper protein involved in t
A:Reference number: Z14322; MUID:98154557; PMID:9490265
A:Accession: T01415
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-531 <MAL>
A:Cross-references: UNIPROT:Q49067; EMBL:AF036949; NID:g2865393; PIDN:AAC39351.1; PID:g2
C:Genetics:
A:Gene: l1guleless2
A:Map position: 9

Query Match      2.2%; Score 8; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      172 DFQPAAS 179
DB      42 DFQPAAS 49

RESULT 22
AB1398
formate dehydrogenase alpha chain homolog lmo2586 [imported] - Listeria monocytogenes (S
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C:Accession: AB1398
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshih, H.
D.; Jones, L.M.; Karsst, U.
Science 294, 849-852, 2001
A:Authors: Krefelt, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tlierer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-995 <GLA>
A:Cross-references: UNIPROT:Q8Y469; GB:NC_003210; PIDN:CAD00664.1; PID:g16412074; GSPDB:
```

```
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2586
C:Superfamily: NAD-dependent formate dehydrogenase alpha subunit; ferredoxin 2(4Fe-4S) h

Query Match      2.2%; Score 8; DB 2; Length 995;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      302 CGGCGCG 309
DB      982 CGGCGCG 989

RESULT 23
AE1773
formate dehydrogenase alpha chain homolog lin2731 [imported] - Listeria innocua (strain '
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C:Accession: AE1773
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshih, H.
D.; Jones, L.M.; Karsst, U.
Science 294, 849-852, 2001
A:Authors: Krefelt, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tlierer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1773
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-995 <GLA>
A:Cross-references: UNIPROT:Q92707; GB:AL592022; PIDN:CAC97957.1; PID:g16415267; GSPDB:G
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: lin2731
C:Superfamily: NAD-dependent formate dehydrogenase alpha subunit; ferredoxin 2(4Fe-4S) h

Query Match      2.2%; Score 8; DB 2; Length 995;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      302 CGGCGCG 309
DB      982 CGGCGCG 989

RESULT 24
S24066
protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 11-Aug-1995 #text_change 21-Jul-2000
C:Accession: S24066; C38269; T52613
R:Partanen, U.; Armstrong, E.; Maekela, T.P.; Korhonen, J.; Sandberg, M.; Renkonen, R.;
Mol. Cell. Biol. 12, 1698-1707, 1992
A:Title: A novel endothelial cell surface receptor tyrosine kinase with extracellular ep
A:Reference number: S24066; MUID:92195316; PMID:1312667
A:Accession: S24066
A:Molecule type: mRNA
A:Residues: 1-1138 <PAR>
A:Cross-references: EMBL:X60957
R:Partanen, U.; Meekela, T.P.; Alitalo, R.; Lehtvaeslajho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A:Reference number: A38268; MUID:91062389; PMID:2247464
A:Accession: C38269
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 981-1034 <PAW>
A:Experimental source: clone JTK14
R:Korhonen, J.; Lahtinen, I.; Halmekyro, M.; Alhonen, L.; Janne, J.; Dumont, D.; Alitalo
Blood 86, 1828-1835, 1995
A:Title: Endothelial-specific gene expression directed by the tie gene promoter in vivo.
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A:Reference number: 152613; MUID:95383653; PMID:7655012
 A:Accession: 152613
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:579347; NID:G1086921; PIDN:AAD14299.1; PID:G4261999
 C:Genetics:
 A:Gene: GDB:TIE; JTK14
 A:Cross-references: GDB:212873; OMIM:600222
 A:Map position: 1p34-1p33
 C:Function:
 A:Description: catalyzes the phosphorylation of a peptide tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin tyf
 C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
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 F:22-1138/Product: protein-tyrosine kinase, receptor-type tie #status predicted <MAT>
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 F:215-255/Domain: EGF homology <EG1>
 F:259-302/Domain: EGF homology <EG2>
 F:306-344/Domain: EGF homology <EG3>
 F:365-428/Domain: immunoglobulin homology <IM2>
 F:449-530/Domain: fibronectin type III repeat homology <FN3A>
 F:542-633/Domain: fibronectin type III repeat homology <FN3B>
 F:642-730/Domain: fibronectin type III repeat homology <FN3C>
 F:761-786/Domain: transmembrane #status predicted <TM>
 F:837-1114/Domain: protein kinase homology <KIN>
 F:845-853/Region: protein kinase ATP-binding motif
 F:43-105,372-426/Dsulfide bonds: #status predicted
 F:83,161,503,596,709/Binding site: carbohydrate (Aen) (covalent) #status predicted
 F:870,887,979/Active site: Lys, Glu, Asp #status predicted

Query Match 2.2% Score 8; DB 1; Length 1138;
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QY 121 ETSTIRG 128
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 Db 700 ETSTIRG 707

RESULT 25

G90831
 Probable endopeptidase [Imported] - Escherichia coli (strain O157:H7, substrain RIMD 05C
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: G90831
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 gaeawara, N.; Yaenunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: G90831
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-153 <NAV>
 A:Cross-references: UNIPROT:Q8X704; GB:BA000007; PIDN:BAR35046.1; PID:G133361087; GSPDB:C
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: Ecsl623
 C:Superfamily: phage PA2 endopeptidase

Query Match 1.9% Score 7; DB 2; Length 153;
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 ELKLANV 290
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 Db 43 ELKLANV 49

Search completed: November 10, 2005, 09:47:35
 Job time : 43 secs

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